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(57) Abstract

The invention provides novel nucleotide sequences located in a gene which encodes a bacterial flagellin antigen, and the use of those nucleotide sequences for the detection of bacteria which express particular flagellin antigens, on the basis of that antigen alone, or in conjunction with the O antigen expressed by that strain.

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Antigens and Their Detection

TECHNICAL FIELD

The invention relates to novel nucleotide sequences located in a gene which encodes a bacterial flagellin antigen, and the use of those nucleotide sequences for the detection of bacteria which express particular flagellin antigens, on the basis of that antigen alone, or in conjunction with the O antigen expressed by that strain.

BACKGROUND ART

The flagellum of many bacteria appears to be made up of a single protein known as flagellin. The serotyping schemes of *E. coli* and *Salmonella enterica* are based on highly variable antigenic surface structures which include the lipopolysaccharide which carries the O antigen and flagellin which is now known to be the carrier of the classical H antigen. In many strains of *S. enterica* there are two loci (*fliC* and *fljB*) which encode flagellin, and a regulatory system which allows one only to be expressed at any time; and which also provides for expression to rapidly alternate between the two forms first identified as two phases (H1 and H2) for the H antigen of most strains. In *E. coli* there are 54 forms of H antigen recognised and until recently they were all thought to be encoded at the *fliC* locus, as has been shown for *E. coli* K-12. However in the 1980s Ratiner [Ratiner Y A "Phase variation of the H antigen in *Escherichia coli* strain Bi327-41, the standard strain for *Escherichia coli* flagellin antigen H3" FEMS Microbiol. Lett 15 (1982) 33-36; Ratiner Y A "Presence of two structural genes determining antigenically different phase-specific flagellins in some *Escherichia coli* strains" FEMS Microbiol. Lett. 19 (1983) 37-41; Ratiner Y A "Two genetic arrangements determining flagellin antigen specificities in two diphasic *Escherichia coli* strains" FEMS Microbiol. Lett. 29 (1985) 317-323; Ratiner Y A "Different alleles of the flagellin gene *hagB* in *Escherichia coli* standard H

test strains" FEMS Microbiol Lett. 48 (1987) 97-104.] showed that in some cases there are two loci and that expression can alternate. The matter was further complicated by a recent paper by Ratiner [Ratiner Y A (1998) "New flagellin-specifying genes in some *Escherichia coli* strains" J. Bacteriol. 180 979-984] showing three loci (*flk*, *fll* and *flm*) for flagellin in addition to *fliC* although the *fljB* locus has not been found in *E. coli*. However *E. coli* strains are normally identified by the combination of one O antigen and one H antigen [and K antigen when present as a capsule (K) antigen], with no problems reported for the vast majority of cases with alternate phases, while *S. enterica* strains are normally identified by the combination of O, H1 and H2 antigens. It is still not clear how widespread in *E. coli* H antigens determined by flagellin genes other than *fliC* are.

Typing is typically carried out using specific antisera. The incidence of pathogenic *E. coli* in association with human and animal disease supports the need for suitable and rapid typing techniques.

DESCRIPTION OF THE INVENTION

In a first aspect, the present invention provides a novel nucleic acid molecule encoding all or part of an *E. coli* flagellin protein.

The present invention provides, for the first time, full length sequence for a flagellin gene for the following *E. coli* type strains: H6 (SEQ ID NO: 8), H9(SEQ ID NO: 11), H10(SEQ ID NO: 12), H14(SEQ ID NO: 15), H18(SEQ ID NO: 18), H23(SEQ ID NO: 22), H51(SEQ ID NO: 50), H45(SEQ ID NO: 43), H49(SEQ ID NO: 48), H19(SEQ ID NO: 19), H30(SEQ ID NO: 29), H32(SEQ ID NO: 31), H26(SEQ ID NO: 25), H41(SEQ ID NO: 39), H15(SEQ ID NO: 16), H20(SEQ ID NO: 20), H28(SEQ ID NO: 27), H46(SEQ ID NO: 44), H31(SEQ ID NO: 30), H34(SEQ ID NO: 33), H43(SEQ ID NO: 41) and H52(SEQ ID NO: 51). Corrected full length sequences have been obtained for H7(SEQ ID NO: 9) and

H12(SEQ ID NO: 14) type strains.

Partial flagellin gene sequence, including the central variable region, has been obtained for the following *E. coli* H type strains: H40(SEQ ID NO: 38), H8(SEQ ID NO: 10), H21(SEQ ID NO: 21), H47(SEQ ID NO: 46), H11(SEQ ID NO: 13), H17(SEQ ID NO: 17), H25(SEQ ID NO: 24), H42(SEQ ID NO: 40), H27(SEQ ID NO: 26), H35(SEQ ID NO: 34), H2(SEQ ID NO: 67), H3(SEQ ID NO: 68), H24(SEQ ID NO: 23), H37(SEQ ID NO: 35), H50(SEQ ID NO: 49), H4(SEQ ID NO: 6), H44(SEQ ID NO: 42), H38(SEQ ID NO: 36), H39(SEQ ID NO: 37), H55(SEQ ID NO: 53), H29(SEQ ID NO: 28), H33(SEQ ID NO: 32), H5(SEQ ID NO: 7), H54(SEQ ID NO: 52) and H56(SEQ ID NO: 54).

Comparison of sequences demonstrates that unique flagellin genes have now been sequenced (partially or completely) for the following *E. coli* H type strains: H1, H2, H3, H5, H6, H7, H9, H11, H12, H14, H15, H18, H19, H20, H21, H23, H24, H25, H26, H27, H28, H29, H30, H31, H32, H33, H34, H35, H37, H38, H39, H41, H42, H43, H45, H46, H48, H49, H51, H52, H54, and H56 and either H8 or H40, H10 or H50 and H4 or H17.

By comparison of these sequences, the present inventors were able to identify specific sequences for each of the above H serotypes.

The present invention also provides *fliC* sequences from 10 different H7 strains, in addition to that from the H7 type strain, and two sequences specific to H7 of O157 and O55 *E. coli* strains.

The present invention encompasses all or part of the flagellin genes sequenced for H2, H3, H5, H6, H9, H11, H14, H18, H19, H20, H21, H23, H24, H25, H26, H27, H28, H29, H30, H31, H32, H33, H34, H35, H37, H38, H39, H41, H42, H43, H44, H45, H46, H47, H48, H49, H51, H52, H54, H55, H56, H8, H40, H15, H10, or H50, H4 and H17 type strains. Of these flagellin genes sequenced, those from the type strains for H8 and H40 are identical, those from type strains H10 and H50, H1 and H12, H38 and H55, H21 and

H47, and H4, H17 and H44 type strains are highly similar.

The invention also encompasses newly provided sequence for H7 and H12 as well as novel primers for the specific amplification of H1, H7, H12 and H48 as well as for the other above mentioned newly sequenced flagellin genes.

By cloning and expression of these sequenced flagellin genes in a *fliC* deletion *E. coli* K-12 strain, and use of anti-H antiserum, we have confirmed the H specificities encoded by 39 falgellin genes. The 39 H specificities are H1, H2, H4, H5, H6, H7, H9, H10, H11, H12, H14, H15, H16, H18, H19, H20, H21, H23, H24, H26, H27, H28, H29, H30, H31, H32, H33, H34, H38, H39, H41, H42, H43, H45, H46, H49, H51, H52, and H56, encoded by flagellin genes obtained from H type strains for H1, H2, H4, H5, H6, H7, H9, H10, H11, H12, H14, H15, H3, H18, H19, H20, H21, H23, H24, H26, H27, H28, H29, H30, H31, H32, H33, H34, H38, H39, H41, H42, H43, H45, H46, H49, H51, H52, and H56 respectively.

The nucleic acid molecules of the invention may be variable in length. In one embodiment they are oligonucleotides of from about 10 to about 20 nucleotides in length. The oligonucleotides of the invention are specific for the flagellin gene from which they are derived and are derived from the central region of the gene. In one embodiment, oligonucleotides in accordance with the present invention, which also include oligonucleotides from the previously sequenced *E. coli* H1, H7, H12 and H48 genes, are those shown in Table 3.

The 45 sequences (see Table 3) provide a panel to which newly sequenced genes can be compared to select specific oligonucleotides for those newly sequenced genes.

In a second aspect the invention provides a method of detecting the presence of *E. coli* of a particular H serotype in a sample, the method comprising the step of specifically hybridising at least one nucleic acid molecule derived from a flagellin gene, wherein the at

least one nucleic acid molecule is specific for a particular flagellin gene associated with the H serotype, to any *E. coli* in the sample which contain the gene, and detecting any specifically hybridised nucleic acid molecules, wherein the presence of specifically hybridised nucleic acid molecules identifies the presence of the H serotype in the sample.

In one preferred embodiment the detection method is a Southern blot method. More preferably, the nucleic acid molecule is labelled and hybridisation of the nucleic acid molecule is detected by autoradiography or detection of fluorescence.

Preferred nucleic acid molecules for the detection of particular flagellin genes are listed in Table 3.

In a third aspect the invention provides a method of detecting the presence of *E. coli* of a particular H serotype in a sample, the method comprising the step of specifically hybridising at least one pair of nucleic acid molecules to any *E. coli* in the sample which contains the flagellin gene for the particular H serotype, wherein at least one of the nucleic acid molecules is specific for the particular flagellin gene associated with the H serotype, and detecting any specifically hybridised nucleic acid molecules, wherein the presence of specifically hybridised nucleic acid molecules identifies the presence of the H serotype in the sample.

In one preferred embodiment the detection method is a polymerase chain reaction method. More preferably, the nucleic acid molecules are labelled and hybridisation of the nucleic acid molecule is detected by electrophoresis.

It is recognised that there may be instances where spurious hybridisation will arise through the initial selection of a sequence found in many different genes but this is typically recognisable by, for instance, comparison of band sizes against controls in PCR gels, and an alternative sequence can be selected.

In a fourth aspect the invention provides a method for detecting the presence of a particular O serotype and H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) specifically hybridising at least one nucleic acid molecule, derived from and specific for a gene encoding a transferase or a gene encoding an enzyme for the transport or processing of a polysaccharide or oligosaccharide unit, the gene being involved in the synthesis of a particular *E. coli* O antigen, to any *E. coli* in the sample which contain the gene;

(b) specifically hybridising at least one nucleic acid molecule derived from and specific for a particular flagellin gene associated with that H serotype, to any *E. coli* in the sample which contain the gene; and

(c) detecting any specifically hybridised nucleic acid molecules.

Preferred nucleic acid molecules for the detection of particular flagellin genes are listed in Table 3.

In one preferred embodiment, the sequence of the nucleic acid molecule specific for the O antigen is specific to the nucleotide sequence encoding the O111 antigen. More preferably, the sequence is derived from a gene selected from the group consisting of *wbdH* (nucleotide position 739 to 1932 of Figure 5), *wzx* (nucleotide position 8646 to 9911 of Figure 5), *wzy* (nucleotide position 9901 to 10953 of Figure 5), *wbdM* (nucleotide position 11821 to 12945 of Figure 5) and fragments of those molecules of at least 10-12 nucleotides in length. Particularly preferred nucleic acid molecules are those set out in Tables 8 and 8A, with respect to the above mentioned genes.

In another preferred embodiment, the sequence of the nucleic acid molecule specific for the O antigen is specific to the nucleotide sequence encoding the O157 antigen. More preferably, the sequence is derived from a gene selected from the group consisting of *wbdN*

(nucleotide position 79 to 861 of Figure 6), *wbdO* (nucleotide position 2011 to 2757 of Figure 6), *wbdP* (nucleotide position 5257 to 6471 of Figure 6), *wbdR* (nucleotide position 13156 to 13821 of Figure 6), *wzx* (nucleotide position 2744 to 4135 of Figure 6) and *wzy* (nucleotide position 858 to 2042 of Figure 6) and fragments of those molecules of at least 10-12 nucleotides in length. Particularly preferred nucleic acid molecules are those set out in Tables 9 and 9A, with respect to the above mentioned genes.

In one preferred embodiment the detection method is a Southern blot method. More preferably, the nucleic acid molecule is labelled and hybridisation of the nucleic acid molecule is detected by autoradiography or detection of fluorescence.

In a fifth aspect the invention provides a method for detecting the presence of a particular O serotype and H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) specifically hybridising at least one pair of nucleic acid molecules, at least one of which is derived from and specific for a gene encoding a transferase or a gene encoding an enzyme for the transport or processing of a polysaccharide or oligosaccharide unit, the gene being involved in the synthesis of the particular *E. coli* O antigen, to any *E. coli* in the sample which contain the gene;

(b) specifically hybridising at least one pair of nucleic acid molecules, at least one of which is derived from and specific for a particular flagellin gene associated with the particular H serotype, to any *E. coli* in the sample which contain the gene; and

(c) detecting any specifically hybridised nucleic acid molecules.

Preferred nucleic acid molecules for the detection of particular flagellin genes are listed in Table 3.

In one preferred embodiment, the sequence of the nucleic acid molecule specific for the O antigen is specific to the nucleotide sequence encoding the O111 antigen. More preferably, the sequence is derived from a gene selected from the group consisting of *wbdH* (nucleotide position 739 to 1932 of Figure 5), *wzx* (nucleotide position 8646 to 9911 of Figure 5), *wzy* (nucleotide position 9901 to 10953 of Figure 5), *wbdM* (nucleotide position 11821 to 12945 of Figure 5) and fragments of those molecules of at least 10-12 nucleotides in length. Particularly preferred nucleic acid molecules are those set out in Tables 8and 8A, with respect to the above mentioned genes.

In another preferred embodiment, the sequence of the nucleic acid molecule specific for the O antigen is specific to the nucleotide sequence encoding the O157 antigen. More preferably, the sequence is derived from a gene selected from the group consisting of *wbdN*(nucleotide position 79 to 861 of Figure 6), *wbdO* (nucleotide position 2011 to 2757 of Figure 6), *wbdP* (nucleotide position 5257 to 6471 of Figure 6), *wbdR* (nucleotide position 13156 to 13821 of Figure 6), *wzx* (nucleotide position 2744 to 4135 of Figure 6) and *wzy* (nucleotide position 858 to 2042 of Figure 6) and fragments of those molecules of at least 10-12 nucleotides in length. Particularly preferred nucleic acid molecules are those set out in Tables 9 and 9A, with respect to the above mentioned genes.

In one preferred embodiment the detection method is a polymerase chain reaction method. More preferably, the nucleic acid molecules are labelled and hybridisation of the nucleic acid molecule is detected by electrophoresis.

The present inventors believe that based on the teachings of the present invention and available information concerning O antigen gene clusters, and through use of experimental analysis, comparison of nucleic acid sequences or predicted protein structures, nucleic acid molecules in accordance with the invention

can be readily derived for any particular O antigen of interest. Suitable bacterial strains can typically be acquired commercially from depositary institutions.

There are currently 166 defined *E. coli* O antigens.

Samples of the 166 different *E. coli* O antigen serotypes are available from Statens Serum Institut, Copenhagen, Denmark.

The inventors envisage rare circumstances whereby two genetically similar gene clusters encoding serologically different O antigens have arisen through recombination of genes or mutation so as to generate polymorphic variants. In these circumstances multiple pairs of oligonucleotides may be selected to provide hybridisation to the specific combination of genes. The invention thus envisages the use of a panel containing multiple nucleic acid molecules for use in the method of testing for O antigen in conjunction with H antigen, wherein the nucleic acid molecules are derived from genes encoding transferases and/or enzymes for the transport or processing of a polysaccharide or oligosaccharide unit including *wzx* or *wzy* genes, wherein the panel of nucleic acid molecules is specific to a particular O antigen. The panel of nucleic acid molecules can include nucleic acid molecules derived from O antigen sugar pathway genes where necessary.

The inventors also found two mutated flagellin genes from H type strains for H35 and H54 which have insertion sequences inserted into normal flagellar genes identical or near identical to that that of the H11 and H21 type strains respectively. Thus, primers for H11 and H21 (listed in Table 3) would also amplify fragments in H35 and H54, which differ in sizes to those in H11 and H21 respectively. The inventors also provide two pairs of primers each for H35 and H54 based on the insertion sequence (see H35 and H54 columns in Table 3). The use of one of them in combination with one of the H11 or H21 primers will generate a PCR band only in H35 or H54 respectively, and this will also differentiate H35 and H54

from H11 and H21 respectively.

The present invention also relates to methods of detecting the presence of particular *E. coli* H antigens or H antigen and O antigen combinations where one or more nucleic acid molecules which generate a particular size fragment indicative of the presence of that H antigen are used or in which the combination of one antigen specific primer for that H antigen with another primer for a related H antigen provides for the detection of the particular H antigen by hybridisation to the relevant gene. Preferably, the H antigen is H11, H21, H35 or H54.

The pairs of nucleic acid molecules where the method of the fifth aspect is used may both hybridise to the relevant H or O antigen gene or alternatively only one may hybridise to the relevant gene and the other to another site.

The inventors recognise in applying the methods of the invention for detecting combinations of O and H antigens to samples, that the methods do not indicate whether a positive result for a particular O and H antigen combination arises because the O and H antigen are present on a single *E. coli* strain present in the sample or are present on different *E. coli* strains present in the sample. Because the ability to identify the presence of *E. coli* strains with particular O and H antigen combinations is highly desirable (due to the relationship between particular combinations and pathogenicity) the determination that a particular combination is present in a sample can be followed by isolation of single colonies and checking whether the they contain the relevant combination by using the same method again or using antibody labelled magnetic beads to separate cells expressing the particular O or H antigen and then testing the isolated cells for the other serotype.

In addition, as mentioned above, the present inventors have established the existence of H7 primers specific to the O157 and O55 serotypes. Using such

primers it is possible to detect particular O and H antigen combinations with the use of H specific nucleic acid molecules.

In a sixth aspect the invention provides a method for detecting the presence of a particular O serotype and H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) specifically hybridising at least one nucleic acid molecule, derived from and specific for a gene encoding a flagellin associated with a particular *E. coli* H antigen serotype to any *E. coli* carrying the gene and present in the sample;

and

(b) detecting the at least one specifically hybridised nucleic acid molecule, wherein the at least one nucleic acid molecule is specific for the particular combination of O and H antigen.

Preferably the combination is O55:H7 or O157:H7.

The ability to detect the O157:H7 combination from a particular H7 primer or pair is of particular use given the association of this combination with pathogenic strains.

In a seventh aspect the present invention provides a method for testing a food derived sample for the presence of one or more particular *E. coli* O antigens and H antigens comprising testing the sample by a method of the fourth, fifth or sixth aspect the invention.

In an eighth aspect the present invention provides a method for testing a faecal derived sample for the presence of one or more particular *E. coli* O antigens and H antigens comprising testing the sample by a method of the fourth, fifth or sixth aspect the invention.

In a ninth aspect the present invention provides a method for testing a patient or animal derived sample for the presence of one or more particular *E. coli* O antigens and H antigens comprising testing the sample by a method of the fourth, fifth or sixth aspect the invention.

Preferably, the method of the seventh, eighth or ninth aspect of the invention is a polymerase chain reaction method. More preferably the oligonucleotide molecules for use in the method are labelled. Even more preferably the hybridised nucleic acid molecules are detected by electrophoresis.

In the above described methods it will be understood that where pairs of nucleic acid molecules are used one of the nucleic acid molecules may hybridise to a sequence that is not from the O antigen transferase, *wzx* or *wzy* gene or the flagellin gene. Further where both hybridise to these genes the O antigen molecules may hybridise to the same or a different one of these genes.

In a tenth aspect the present invention provides a kit for identifying the H serotype of *E. coli*, the kit comprising:

at least one nucleic acid molecule derived from and specific for an *E. coli* flagellin gene.

In an eleventh aspect the present invention provides a kit for identifying the H and O serotype of *E. coli*, the kit comprising:

(a) at least one nucleic acid molecule derived from and specific for an *E. coli* flagellin gene; and

(b) at least one nucleic acid molecule derived from and specific for a gene encoding a transferase or a gene encoding an enzyme for the transport or processing of a polysaccharide or oligosaccharide unit, the gene being involved in the synthesis of a particular *E. coli* O antigen.

The nucleic acid molecules may be provided in the same or different vials. The kit may also provide in the same or separate vials a second set of specific nucleic acid molecules.

Particularly preferred nucleic acid molecules for inclusion in the kits are those specified in Tables 3, 8, 8A, 9 and 9A as described above.

DEFINITIONS

In this specification, we have used term "flagellin gene" in many cases where previously one would have used "*fliC*", to allow for the uncertainty as to locus introduced by recent observations. However, uncertainty as to the locus does not alter the fact that most *E. coli* strains express a single H antigen and that a single flagellin gene sequence per strain is required to give the genetic basis for H antigen variation . Any use of the name *fliC* in this specification where a different locus is later shown to be involved would not affect the validity of conclusions drawn regarding application of information based on the sequence, where the conclusions do not relate to the map position. Thus it is generally the nucleic acid molecule itself which is of importance rather than the name attributed to the gene. When it is known or suspected that the gene encoding the H antigen is not in the *fliC* locus, we use the term flagellin rather than *fliC*.

The phrase, "a nucleic acid molecule derived from a gene" means that the nucleic acid molecule has a nucleotide sequence which is either identical or substantially similar to all or part of the identified gene. Thus a nucleic acid molecule derived from a gene can be a molecule which is isolated from the identified gene by physical separation from that gene, or a molecule which is artificially synthesised and has a nucleotide sequence which is either identical to or substantially similar to all or part of the identified gene. While some workers consider only the DNA strand with the same sequence as the mRNA transcribed from the gene, here either strand is intended.

Transferase genes are regions of nucleic acid which have a nucleotide sequence which encodes gene products that transfer monomeric sugar units.

Flippase or *wzx* genes are regions of nucleic acid which have a nucleotide sequence which encodes a gene

product that flips oligosaccharide repeat units generally composed of three to six monomeric sugar units to the external surface of the membrane.

Polymerase or *wzy* genes are regions of nucleic acid which have a nucleotide sequence which encodes gene products that polymerise repeating oligosaccharide units generally composed of 3-6 monomeric sugar units.

The nucleotide sequences provided in this specification are described as anti-sense sequences. This term is used in the same manner as it is used in Glossary of Biochemistry and Molecular Biology Revised Edition, David M. Glick, 1997 Portland Press Ltd., London on page 11 where the term is described as referring to one of the two strands of double-stranded DNA usually that which has the same sequence as the mRNA. We use it to describe this strand which has the same sequence as the mRNA.

NOMENCLATURE

Synonyms for E. coli O111 *rfb*

Current names	Our names	Bastin et al. 1991
wbdH	orf1	
gmd	orf2	
wbdI	orf3	orf3.4*
manC	orf4	rfbM*
manB	orf5	rfbK*
wbdJ	orf6	orf6.7*
wbdK	orf7	orf7.7*
wzx	orf8	orf8.9 and rfbX*
wzy	orf9	
wbdL	orf10	
wbdM	orf11	

* Nomenclature according to Bastin D.A., *et al*. 1991 "Molecular cloning and expression in Escherichia coli K-12 of the *rfb* gene cluster determining the O antigen of an E. coli O111 strain". *Mol. Microbiol*. 5:9 2223-2231.

Other Synonyms

wzy	rfc
wzx	rfbX
rmlA	rfbA
rmlB	rfbB
rmlC	rfbC
rmlD	rfbD
glf	orf6*
wbbI	orf3#, orf8* of E. coli K-12

wbbJ	orf2#, orf9* of E. coli K-12
wbbK	orf1#, orf10* of E. coli K-12
wbbL	orf5#, orf 11* of E. coli K-12

\# Nomenclature according to Yao, Z. And M. A. Valvano 1994. "Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (rfb) of Eschericia coli K-12 W3110: identification of genes the confer groups-specificty to Shigella flexineri serotypes Y and 4a". J. Bacteriol. 176: 4133-4143.

* Nomenclature according to Stevenson et al. 1994. "Structure of the O-antigen of E. coli K-12 and the sequence of its rfb gene cluster". J. Bacteriol 176: 4144-4156.

- The O antigen genes of many species were given rfb names (rfbA etc) and the O antigen gene cluster was often referred to as the rfb cluster. There are now new names for the rfb genes as shown in the table. Both terminologies have been used herein, depending on the source of the information.

In the claims that follow and in the summary of the invention, except where the context requires otherwise due to express language or necessary implication, the word "comprising" is used in the sense of "including", i.e. the features specified may be associated with further features in various embodiments of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows *Eco* R1 restriction maps of cosmid clones pPR1054, pPR1055, pPR1056, pPR1058, pPR1287 which are subclones of *E. coli* O111 O antigen gene cluster. The thickened line is the region common to all clones. Broken lines show segments that are non-contiguous on the chromosome. The deduced restriction map for *E. coli* strain M92 is shown above.

Figure 2 shows a restriction mapping analysis of *E. coli* O111 O antigen gene cluster within the cosmid clone pPR1058. Restriction enzymes are: (B: *Bam*H1; Bg: *Bgl*II, E: *Eco*R1; H: *Hind*III; K: *Kpn*I; P: *Pst*I; S: *SalI* and X: *Xho*1. Plasmids pPR1230, pPR1231, and pPR1288 are deletion derivatives of pPR1058. Plasmids pPR 1237, pPR1238, pPR1239 and pPR1240 are in pUC19. Plasmids pPR1243, pPR1244, pPR1245, pPR1246 and pPR1248 are in pUC18, and pPR1292 is in pUC19. Plasmid pPR1270 is in

pT7T319U. Probes 1, 2 and 3 were isolated as internal fragments of pPR1246, pPR1243 and pPR1237 respectively. Dotted lines indicate that subclone DNA extends to the left of the map into attached vector.

Figure 3 shows the structure of *E. coli* O111 O antigen gene cluster.

Figure 4 shows the structure of *E. coli* O157 O antigen gene cluster.

Figure 5 shows the nucleotide sequence (SEQ ID NO: 45) of the *E. coli* O111 O antigen gene cluster. Note: (1) The first and last three bases of a gene are underlined and of italic respectively.; (2) The region which was previously sequenced by Bastin and Reeves 1995 "Sequence and anlysis of the O antigen gene (rfb) cluster of *Escherichia coli O*111" Gene 164: 17-23 is marked.

Figure 6 shows the nucleotide sequence (SEQ ID NO: 56) of the *E. coli* O157 O antigen gene cluster. Note: (1) The first and last three bases of a gene (region) are underlined and of *italic* respectively (2) The region previously sequenced by Bilge et al. 1996 "Role of the *Escherichia coli* O157-H7 O side chain in adherence and analysis of an rfb locus". Inf. and Immun 64:4795-4801 is marked.

Figures 7 to 9 show the nucleotide sequences (SEQ ID NOS: 66 to 68 respectively) obtained for flagellin genes from *E. coli* type strains for H1 to H3 respectively. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figures 10 to 18 show the nucleotide sequences (SEQ ID NOS: 6 to 14 respectively) obtained for flagellin genes from *E. coli* type strains for H4 to H12 respectively. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figures 19 and 20 show the nucleotide sequences (SEQ ID NOS: 15 to 16 respectively) obtained for flagellin genes from *E. coli* type strains for H14 and H15 respectively. The primer positions listed in Table 3 are

based on treating the first nucleotide of each of these sequences as No. 1.

Figures 22 and 26 show the nucleotide sequences (SEQ ID NOS: 17 to 21 respectively) obtained for flagellin genes from *E. coli* type strains for H17 and H21 respectively. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figures 27 to 39 show the nucleotide sequences (SEQ ID NOS: 22 to 34) obtained for flagellin genes from *E. coli type strains for* H23 to H35 respectively. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figures 40 to 49 show the nucleotide sequences (SEQ ID NOS: 35 to 44) obtained for flagellin genes from *E. coli* type strains for H37 to H46 respectively. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figures 50 to 55 show the nucleotide sequences (SEQ ID NOS: 46 to 51) obtained for flagellin genes from *E. coli* type strains for H47 to H52 respectively. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figures 56 to 58 show the nucleotide sequences (SEQ ID NOS: 52 to 54) obtained for flagellin genes from *E. coli* type strains for H54 to H56 respectively. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figure 59 shows the nucleotide sequence (SEQ ID NO: 55) obtained for the flagellin gene from *E. coli* H7 strain M1179. The primer positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figures 60 to 68 show the nucleotide sequences (SEQ ID NOS: 57 to 65 respectively) obtained for flagellin genes from E. coli strains M1004, M1211, M1200, M1686, M1328, M917, M527, M973, and M918 respectively. The primer

positions listed in Table 3 are based on treating the first nucleotide of each of these sequences as No. 1.

Figure 69 shows the nucleotide sequence (SEQ ID NO: 1) of the *fliC* gene and DNA flanking the *fliC* gene from the H25 type strain.

Figure 70A shows the nucleotide sequence (SEQ ID NO: 2) obtained from the 5′ end of the insert of plasmid pPR1989. The insert of plasmid pPR1989 encodes the second flagellin gene of the H55 type strain.

Figure 70B shows the nucleotide sequence (SEQ ID NO: 3) obtained from the 3′ end of the insert of plasmid pPR1989. The insert of plasmid pPR1989 encodes the second flagellin gene of the H55 type strain.

Figure 71 shows the nucleotide sequence (SEQ ID NO:4) obtained from the 5′ end of the insert of plasmid pPR1993. The insert of plasmid pPR1993 encodes the second flagellin gene of the H36 strain.

Figure 72 shows the nucleotide sequence (SEQ ID NO:5) obtained from the 3′ end of the insert of plasmid pPR1993. The insert of plasmid pPR1993 encodes the second flagellin gene of the H36 type strain.

Figure 73 A shows the sequence of polylinker and the SD sequence of plasmid pTrc99A.

Figure 73B shows the sequence of the junction region between the SD sequence and the start of flagellin gene in the plasmids used for the expression of flagellin genes.

BEST METHOD OF CARRYING OUT THE INVENTION

In carrying out the methods of the invention with respect to the testing of particular sample types including samples from food, patients, animals and faeces the samples are prepared by routine techniques routinely used in the preparation of such samples for DNA based testing. The steps for testing the samples using particular nucleic acid molecules in assay formats such as Southern blots and PCR are performed under routinely determined conditions appropriate to the sample and the

nucleic acid molecules.

H antigen

Materials and Methods

1. Bacterial strains and plasmid:

There are 54 H types in *E. coli* [Ewing, W.H.: Edwards and Ewing's identification of the *Enterobacteriaceae*., Elsevier Science Publishers, Amsterdam, The Netherlands, 1986]: note H antigens from 1 to 57 were listed and that 13, 22 and 57 are not valid. All the standard H type strains except H16 were obtained from the Institute of Medical and Veterinary Science, Adelaide, Australia. The primary stocks are hold at the Statens Serum Institut, Copenhagen, Denmark.
The additional H7 strains used are listed in Table 1.

We do not have the type strain for H16. It is known that the H3 type strain is biphasic and can also express the H16 flagellin gene [Ratiner, Y. A. (1985) "Two genetic arrangements determining flagellar antigen specificities in two diphasic *E. coli* strains. FEMS Microbiol Lett 19: 317-323]. We have sequenced and cloned the H16 flagellin gene from the H3 type strain (see below).

E. coli K-12 strain C600 *hsm hsr fliC::Tn10* [Kuwajiwa, G. (1988) "Flagellin domain that affects H antigenicity of E. coli K-12" J. Bacteriol. 170; 485-488] (laboratory stock no. M2126) was obtained from Dr Benita Westerlund-Wikstrom of the Department of Biosciences, University of Helsinkin, Finland. *E. coli* K-12 strain EJ2282 (laboratory no. P5560) is a *fliC* deletion strain, and was obtained from Dr Masatoshi Enomoto of the Department of Biology, Okayama University, Japan [Tominaga, A. M. A.-H. Mahmound, T. Mokaihara and M. Enomoto (1994) "Molecular characterization of intact but cryptic, flagellin genes in the genus *Shigella*.: Mol. Microbiol. 12: 277-285].

Plasmid pTrc99A was purchased from Pharmacia LKB (Melbourne, VIC, Australia).

2. Antisera

Antisera against H1, H3, H8, H14, H15, H17, H23, H24, H25, H26, H29, H30, H31, H32, H33, H35, H36, H37, H38, H39, H43, H44, H46, H47, H48, H49, H52, H53, H54, H55, and H56 were obtained from the Institute of Medical and veterinary Science, Adelaide, Australia. Antisera against H2, H4, H5, H6, H7, H9, H10, H11, H12, H16, H18, H19, H20, H21, H27, H28, H34, H40, H41, H42, H45, and H51 were obtained from Denka Seiken Co., Ltd, Tokyo, Japan.

Antisera to type H50 was not available from any known source.

The antisera available were checked against the appropriate type strains to confirm the specificities of both flagellin H antigen and H antisera: 52 sera (all those except anti-H16 serum listed above) gave a positive reaction with the corresponding type strains for that serum.

3. Agglutination test:

Bacteria from 1 ml of an overnight culture grown in Luria broth (Difco Tryptone, 10g/l; Difico yeast extract, 5g/l; NaCl, 0.5 g/l; pH 7.2) at 30oC was centrifuged (4000 rpm/10 min) and the bacteria pellet resuspended in 100 ml of saline. The agglutination test was carried out by mixing equal volumes (5 ml) of both the cells and antiserum on a slide. The slide was rocked for 1 minute and then observed for agglutination. For all agglutination tests, saline containing no antiserum was mixed with cells to be used as a negative control.

For testing the H specificities of strain M2126 or strain P5560 carrying plasmid containing cloned flagellin genes, cells of M2126 or P5560 were used as an additional negative control.

All agglutination tests were first carried out using undiluted antisera (note that the antisera we used have been diluted before reaching our hands), except for anti-

H11, anti-H34, anti-H52 and anti-H26 serum for which we used 1:10 dilutions to avoid background agglutination. In cases for which cross-reactions have been reported, we carried out agglutination tests using serial dilutions of sera (see section 10.1)

4. Motility test:

The motility of strain M2126 or strain P5560 carrying cloned flagellin genes was examined microscopically. 1 ml of overnight culture grown in Luria broth (Difco Tryptone, 10g/l; Difico yeast extract, 5g/l; NaCl, 0.5 g/l; pH 7.2) at 30oC was inoculated into 10 ml of Luria broth, and the culture was shaken at 100 rpm at 30oC to early log phase (OD 625 = 0.2). A loopful of culture was placed on a slide and examined under a microscope. Motility of individual cells was easily distinguished from Brownian movement and streaming, and presence or absence of motility recorded.

5. Isolation of chromosomal DNA:

Chromosomal DNA from all the 53 H type strains and the strains listed in Table 1 was isolated using the Promega Genomic isolation kit (Madison WI USA). Each chromosomal DNA sample was checked by gel electrophoresis of the DNA and by PCR amplification of the *mdh* gene using oligonucleotides based on the *E. coli* K-12 *mdh* gene [Boyd, E.F., Nelson, K., Wang, F.-S., Whittam, T.S. and Selander, R.K.: Molecular genetic basis of allelic polymorphism in malate dehydrogenase (*mdh*) in natural populations of *Escherichia coli* and *Salmonella enterica*. Proc. Natl. Acad. Sci. USA 91 (1994) 1280-1284].

6. PCR amplification of flagellin gene:

Flagellin genes from different strains were first PCR amplified using one of the following four pairs of oligonucleotides:

#1285 (5'-atggcacaagtcattaatac) and

#1286 (5'-ttaaccctgcagtagagaca);

#1417 (5'-ctgatcactcaaaataatatcaac) and
#1418 (5'-ctgcggtacctggttggc);
#1431 (5'-atggcacaagtcattaatacccaac) and
#1432 (5'-ctaaccctgcagcagagaca):
#1575 (5'-gggtggaaacccaatacg) and
#1576(5'-gcgcatcaggcaatttgg)

PCR reactions were carried out under the following conditions: denaturing, 94°C/30'; annealing, temperature varies (refer to Table 2)/30'; extension, 72°C/1'; 30 cycles. The PCR product was purified using the Promega Wizard PCR purification kit (Madison WI USA) before being sequenced.

The H36 and H53 type strains gave two PCR bands using primer pairs #1431/#1432 and #1417/#1418 respectively, and were not sequenced.

7. Enzymes and buffers:

Restriction endonucleases and DNA T4 ligase were purchased from Boehringer Mannheim (Castle Hill, NSW, Australia). Restriction enzymes were used in the recommended commercial buffer.

8. Sequencing of the flagellin genes:

Each PCR product was first sequenced using the oligonucleotide primers used for the PCR amplification. Primers based on the obtained sequence were then used to sequence further, and this procedure was repeated until the entire PCR product was sequenced.

The sequencing reactions were performed using the DyeDeoxy Terminator Cycle Sequencing method (Applied Biosystems, CA, USA), and reaction products were analysed using fluorescent dye and an ABI377 automated sequencer (CA, USA).

Sequence data were processed and analysed using Staden programs [Sacchi CT, Zanella R C, Caugant D A, Frasch C E, Hidalgo N T, Milagres L G, Pessoa L L, Ramos S R, Camargo M C C and Melles C E A "Emergence of a new

clone of serogroup C *Neisseria meningitidis* in Sao Paulo, Brazil" J. Clin. Microbiol. 30 (1992) 1282-1286;
Staden, R.: Automation of the computer handling of gel reading data produced by the shotgun method of DNA sequencing. Nucl. Acids Res. 10 (1982a) 4731-4751;
Staden, R.: An interactive graphics program for comparing and aligning nucleic acid and amino acid sequences. Nucl. Acids Res. 10 (1982b) 2951-2961;
Staden, R.: Computer methods to locate signals in nucleic acid sequences. Nucl. Acids Res. 12 (1984a) 505-519;
Staden, R.: Graphic methods to determine the function of nucleic acid sequences. A summary of ANALYSEQ options. Nucl. Acids Res. 12 (1984b) 521-538;
Staden, R.: The current status and portability of our sequence handling software. Nucl. Acids Res. 14 (1986) 217-231].

We were able to PCR amplify flagellin genes from H type strains for H7, 23, 12, 51, 45, 49, 19, 9, 30, 32, 26, 41, 15, 20, 28, 46, 31, 14, 18, 6, 34, 48, 43, 10, 52, and also from H7 strains m1004, m527, m1686, m1211, m1328, m973, m1179, m1200, m917, and m918 using primers #1575 and #1576 which are based on sequences 51-34 bp upstream and 37-54 bp downstream of start and end of the *E. coli* K-12 *fliC* gene respectively. Thus, the full sequence of the flagellin gene from these strains was obtained and the use of flanking sequence for primers makes it highly likely that they are at the *fliC* locus.

For other strains, we were only able to amplify the *flagellin* gene using one or more of the other three pairs of primers, which are based on sequence within the *fliC* gene, and thus only partial sequence was obtained. These amplicons may be of the *fliC* gene or one of the alternative flagellin genes. The flagellin gene sequences from H type strains for H40, 8, 21, 47, 11, 27, 35, 2, 3, 24, 37, 50, 4, 44, 38, 55, 29, 33, 5, and 56 obtained are lacking 18 and 14 codons at 5' and 3' ends respectively. The flagellin gene sequence of H39 obtained using primers

#1285/#1286 lacks 18 and 19 codons at 5′ and 3′ ends respectively. The flagellin gene sequence of H type strains of H17, 25 and 42 lack 23 and 21 codons at 5′ and 3′ ends respectively. The flagellin gene sequence of the H type strain for H54 lacks 23 and 12 codons at the 5′ and 3′ ends respectively. There is very little variation in the sequence at the two ends of flagellin genes and antigenic variation is due to variation in the central region of the gene. The absence of sequence for the ends of some of the flagellin genes is not important for the purpose of the present invention relating to the detection of antigenic variation by DNA sequence based means.

The *fliC* genes from H type strains of H1, H7 and H12 have been sequenced previously [Schoenhals, G. and Whitfield, C.: Comparative analysis of flagellin sequences from *Escherichia coli* strains possessing serologically distinct flagellar filaments with a shared complex surface pattern. J. Bacteriol. 175 (1993) 5395-5402] and we did not sequence the gene from the H1 strain.

We have sequenced *fliC* genes from a set of H7 strains with different O antigens, including that of *fliC* from the H7 type strain as one of the set: we have found four differences from the published H7 sequence (GenBank accession number L07388) which we believe are due to errors in the published sequence.

We have also re-sequenced the *fliC* gene from the H12 type strain, and have found one difference from the published H12 sequence (GenBank accession number L07389) which we believe is due to an error in the published sequence.

The flagellin genes from type strains H35 and H54 were also amplified using primers #1431/#1432, which are based on sequence within the *fliC* gene. Sequence data revealed that these two genes would be non-functional due to insertion sequence inserted in the middle of them. We have sequenced them to facilitate selection of primers for the functional flagellin genes.

9. Cloning of flagellin genes

DNA was digested for 2 hr at 37°C with appropriate restriction enzyme(s). The reaction product was then extracted once with phenol, and twice with ether. DNA was precipitated with 2 vols of ethanol and resuspended in water before the ligation reaction was carried out. Ligation was carried out O/N at 4°C and the ligated DNA was electroporated into one of the *E. coli fliC* mutant strains.

9.1. Cloning of flagellin genes from type strains for H1, H2, H3, H5, H6, H7, H9, H10, H11, H12, H14, H15, H18, H19, H20, H21, H24, H26, H27, H28, H29, H31, H34, H38, H39, H41, H42, H43, H45, H46, H49, H51, H52, and H56:

The full flagellin gene was PCR amplified using primers #1868 and #1870 (Table 3A). Both these primers are based on the sequences of the H7 flagellin gene of the H7 type strain. #1868 is the 5' primer: there is an *Nco*I site incorporated into the primer (Table 3B) and the flagellin gene starts at base 3 of the *Nco*I site. The 3' primer #1870 has a *Bam*HI site incorporated downstream of the stop codon of the flagellin gene (Table 3B). PCR reactions were carried out under the following conditions: denaturing, 94oC/30'; annealing, temperature varies (refer to Table 3A)/30'; extension, 72oC/1'; 30 cycles. The PCR product was purified using the Promega Wizard PCR purification kit (Madison WI USA) before being digested by restriction enzymes *Nco*I and *Bam*HI and cloned into the *Nco*I/*Bam*HI sites of plasmid pTrc99A.

Plasmid pTrc99A has a strong *trc* promoter upstream of the polylinker. Downstream of the promoter, it contains the ribosome binding site (SD sequence, see Fig 73) which is located 8bp upstream of the ATG site within the *Nco*I site. The polylinker and the SD sequence of pTrc99A are shown in Fig 73.

The plasmids generated were given pPR numbers, and

they are listed in Table 3A. In these plasmids, the expression module consists of the *trc* promoter, the SD sequence, and the full flagellin gene. The sequence of the junction region between the SD sequence and the start of flagellin gene is shown in Fig 73.

For flagellin genes from type strains for H6, H7, H9, H10, H12, H14, H18, H19, H20, H26, H28, H31, H41, H43, H45, H46, H49, H51, and H52, we have the full sequence for each gene and the primer sequences (#1868 and #1870) are conserved among them. The cloned genes therefore have the same sequence as those from the type strains.

For flagellin genes from type strains for H1, H15 and H34, we also have the full sequence. The previously published sequence of the flagellin gene from the H1 type strain was extracted from GenBank (accession number L07387) and used. Primer #1868 is conserved in all three. But, primer #1870 has the third base of the fifth last codon in the H1 sequence changed from A to G, and the third base of the second last codon changed from C to T in the H15 and H34 sequences: these changes did not change the amino acid coded, so the cloned genes encode the same gene products as those of the type strains.

For flagellin genes from type strains for H2, H3, H5, H11, H21, H24, H27, H29, H38, H39, H42, and H56, we do not have the full sequences. In the plasmids carrying genes from these type strains, the expression module consists of the *trc* promoter, the SD sequence, and the full flagellin gene with the first and the last 21 base pairs being determined by the primer sequences which are based on the H7 flagellin gene of the H7 type strain. The sequence of the junction region between the SD sequence and the start of flagellin gene is shown in Fig 73.

9.2. Cloning of the flagellin gene from type strain of H23:

The full flagellin gene was PCR amplified using primers #1868 and #1869 (Table 3A). #1868 is the 5′

primer: there is an *Nco*I site incorporated into the primer (Table 3B) and the flagellin gene starts at base 3 of the *Nco*I site. The 3′ primer #1869 has a *Sal*I site incorporated downstream of the stop codon of the flagellin gene (Table 3B). PCR reactions were carried out under the following conditions: denaturing, 94oC/30′; annealing, 55oC/30′; extension, 72oC/1′; 30 cycles. The PCR product was purified using the Promega Wizard PCR purification kit (Madison WI USA) before being digested by restriction enzymes *Nco*I and SalI and cloned into the *Nco*I/SalI sites of plasmid pTrc99A to give plasmid pPR1942.

Plasmid pTrc99A has a strong *trc* promoter upstream of the polylinker. Downstream of the promoter, it contains the ribosome binding site (SD sequence, see Fig 73) which is located 8bp upstream of the ATG site within the *Nco*I site. The polylinker and the SD sequence of pTrc99A are shown in Fig 73.

The expression module of pPR1942 consists of the *trc* promoter, the SD sequence, and the full flagellin gene. The sequence of the junction region between the SD sequence and the start of flagellin gene is shown in Fig 73.

9.3. Cloning of flagellin genes from type strains of H30, H32 and H33:

The full flagellin gene was PCR amplified using primers #1868 and #1871 (Table 3A). #1868 is the 5′ primer: there is an *Nco*I site incorporated into the primer (Table 3B) and the flagellin gene starts at base 3 of the *Nco*I site. The 3′ primer #1871 has a *Pst*I site incorporated downstream of the stop codon of the flagellin gene (Table 3B). PCR reactions were carried out under the following conditions: denaturing, 94oC/30′; annealing, temperature varies (refer to Table 3A)/30′; extension, 72oC/1′; 30 cycles. The PCR product was purified using the Promega Wizard PCR purification kit (Madison WI USA) before being digested by restriction enzymes *Nco*I and *Pst*I

and cloned into the *Nco*I/*Pst*I sites of plasmid pTrc99A.

Plasmid pTrc99A has a strong trc promoter upstream of the polylinker. Downstream of the promoter, it contains the ribosome binding site (SD sequence, see Fig 73) which is located 8bp upstream of the ATG site within the *Nco*I site. The polylinker and the SD sequence of pTrc99A are shown in Fig 73.

For flagellin genes from type strains for H30 and H32, we have the full sequence. Primer #1868 sequence is conserved in both of them. But, primer #1871 has the third base of the fourth last codon in both sequences changed from G to A to remove a *Pst*I site (see Table 3B): this change did not change the amino acid coded. The expression module consists of the *trc* promoter, the SD sequence, and the full flagellin gene coding for a gene product which is same as that of the type strain. The sequence of the junction region between the SD sequence and the start of flagellin gene is shown in Fig 73.

We do not have the full sequence for the flagellin gene from the H33 type strain. In the plasmid containing the H33 type strain gene, the expression module consists of the *trc* promoter, the SD sequence, and the full flagellin gene with the first and the last 21 base pairs been determined by the primer sequences which were used for the cloning of H30 and H32. The sequence of the junction region between the SD and the start of flagellin gene is shown in Fig 73.

9.4. Flagellin genes from type strains for H4 and H17:

For the flagellin genes of H4 and H17 type strains the full sequence was not obtained, and the sequenced parts were PCR amplified and cloned into plasmid pPR1951 to give in each case a gene in which the first 26 and the last 31 codons are based on the sequence of the H7 flagellin gene of the H7 type strain.

9.4.1 *Construction of expression plasmid vector*

pPR1951:

The first 26 codons of the H7 flagellin gene was first PCR amplified using primers #1868 and #1872 (Table 3B). #1868 is the 5' primer: there is an *Nco*I site incorporated into the primer (Table 3B) and the flagellin gene starts at base 3 of the *Nco*I site. Primer #1872 was made to have the last two codons (codons 25 and 26) changed from CTG TCG (Leucine and Serine) to GGA TCC (Glycine and Serine) to generate a *Bam*HI site. This PCR fragment was digested with *Nco*I and *Bam*HI before being cloned into the *Nco*I/*Bam*HI sites of pTrc99A to make plasmid pPR1949.

The last 31 codons (including the stop codon) of the H7 flagellin gene was PCR amplified using primers #1884 and #1871 (Table 3A). The 5' primer, #1884, has the first two of the 31 codons changed from TCG AAA (Serine and Lysine) to TCT AGA (Serine and Arginine) to generate a *Xba*I site (Table 3B). The 3' primer #1871 has a *Pst*I site incorporated downstream of the stop codon (Table 3B). This PCR fragment was digested with *Xba*I and *Pst*I, and then cloned into the *Xba*I/*Pst*I sites of pPR1949 to make plasmid pPR1951.

9.4.2 Cloning of flagellin genes from the H4 and H17 type strains:

The central regions of flagellin genes from type strains H4 and H17 were PCR amplified using primers #1878 and #1885 (Table 3B), which have a *Bam*HI and a *Xba*I incorporated at their ends respectively. PCR reactions were carried out under the following conditions: denaturing, 94oC/30'; annealing, 65oC/30'; extension, 72oC/1'; 30 cycles. The PCR product was purified using the Promega Wizard PCR purification kit (Madison WI USA) before being digested by restriction enzymes *Bam*HI and *Xba*I and cloned into the *Xba*I/*Bam*HI sites of plasmid pPR1951 to make plasmids pPR1955 (H4) and pPR1957 (H17).

The expression module of plasmids pPR1955 and pPR1957

consists of the *trc* promoter, the SD sequence, the first 24 codons of the H7 flagellin gene (of the H7 type strain), 2 codons encoding Glycine and Serine, 292 or 293 codons of the central region based on the flagellin gene obtained from the H4 or H17 type strain respectively, 2 codons encoding Serine and Arginine, and then the last 29 codons of the H7 flagellin gene (of the H7 type strain).

10. Expression of flagellin gene plasmids in E. coli strains lacking the fliC gene, and identification of the H antigens encoded by these plasmids:

Plasmids carrying flagellin genes as described in section **9** (see Table 3A for a list) were electroporated into strains M2126 or P5560. Strains M2126 and P5560 do not have functional *fliC* genes, and are not motile when examined under a microscope. Transformants carrying any of the plasmids listed in Table 3A are motile when examined under a microscope. Thus, the flagellin genes in all of the plasmids are expressed.

The antigenic specificity of the flagellin of each transformant was then determined by slide agglutination.

10.1 Flagellin genes from type strains for H2, H5, H6, H7, H9, H11, H14, H15, H18, H19, H20, H21, H23, H24, H26, H27, H28, H29, H30, H31, H32, H33, H34, H39, H41, H42, H43, H45, H46, H49, H51, H52, and H56:

As shown in Table 3A, strains with plasmids carrying these flagellin genes expressed the same H antigen as their respective flagellin parent strain.

For flagellin specificities H2, H5, H6, H7, H9, H14, H15, H18, H19, H20, H23, H24, H26, H27, H28, H29, H31, H33, H39, H51, H52, and H56, there was no cross reaction reported between these flagellins and flagellin antisera for other H antigens [Ewing, W. H.: Edwards and Ewing's identification of the *Enterobacteriaceae*., Elsevier Science Publishers, Amsterdam, The Netherlands, 1986], and we conclude that we have in each case sequenced the gene

encoding the flagellin of the expected specificity from the respective type strain.

It has been observed that cross reactions exist between some type strains and certain antisera at different levels of dilution (of the antisera), being H11 with anti-H21 and anti-H40, H21 with anti-H11, H30 with anti-H32, H32 with anti-H30, H34 with anti-H24 and anti-H31, H41 with anti-H37 and anti-H39, H42 with anti-H6, H43 with anti-H37, H45 with anti-H20, H46 with anti-H17, and H49 with anti-H39 [Ewing, W. H.: Edwards and Ewing's identification of the *Enterobacteriaceae.*, Elsevier Science Publishers, Amsterdam, The Netherlands, 1986]. We have tested strain M2126 or strain P5560 carrying plasmids containing flagellin genes obtained from each of these type strains (H11, H21, H30, H32, H34, H41, H42, H43, H45, H46, and H49) with the appropriate cross-reacting antisera.

For strain M2126 or strain P5560 carrying plasmids containing flagellin genes obtained from type strains H11, H34, H41, H42, H43, H45, H46, and H49, no cross reaction was found. We conclude that we have in each case sequenced the gene coding the flagellin of the expected specificity from the respective type strain.

Cross reaction was observed for strain P5560 carrying plasmid pPR1948 (containing the flagellin gene obtained from the H30 type strain) with anti-H32 serum, strain P5560 carrying pPR1940 (containing the flagellin gene obtained from the H32 type strain) with anti-H30 serum , and strain M2126 carrying plasmid pPR1995 (containing the flagellin gene obtained from the H21 type strain) with anti-H11 serum.

We note that the reported cross reactions between the H30 type strain and anti-H32, the H32 type strain and anti-H30, and the H21 type strain and anti-H11 happened at a higher level of dilution (of antisera) than for all other type strains with the antisera mentioned above [Ewing, W. H.: Edwards and Ewing's identification of the

Enterobacteriaceae., Elsevier Science Publishers, Amsterdam, The Netherlands, 1986]. We conclude that except for these three cases, the antiserum used were supplied at a dilution which did not exhibit cross reactions. For the three strains carrying flagellin genes cloned form type strains for H30, H32, and H21, it was necessary to further dilute the antiserum.

Strain P5560 carrying plasmid pPR1948 (containing the flagellin gene obtained from the H30 type strain) agglutinates with anti-H30 serum when the antiserum is diluted to 1:60, but agglutinates with anti-H32 serum only at a dilution of 1:10 and not at a 1:20 dilution (note that the antisera we used have been diluted before reaching our hands). In contrast, strain P5560 carrying plasmid pPR1940 (containing flagellin gene obtained from the H32 type strain) agglutinates with anti-H32 serum when the antiserum is diluted at 1:100, but agglutinates with anti-H30 serum only at a 1:10 dilution and not at a 1:10 dilution. Thus, we conclude that the flagellin genes we sequenced from type strains for H30 and H32 encode flagellins of H30 and H32 specificities respectively.

Strain M2126 carrying plasmid pPR1995 (containing the flagellin gene obtained from the H21 type strain) agglutinates with anti-H21 serum when the antiserum is diluted to 1:40, but agglutinates only with undiluted anti-H11 serum and not at a 1:10 dilution (note that the antisera we used have been diluted before reaching our hands). In contrast, strain M2126 carrying plasmid pPR1981 (containing flagellin gene obtained from the H11 type strain) did not agglutinate with anti-H21 serum. Thus, we conclude that the flagellin genes we sequenced from type strains for H21 encodes flagellin of H21 specificity.

10.2 Flagellin genes from type strains of H1 and H12:

These two genes are very similar in sequence, with 8 a.a difference between the gene products. It has been

known that some cross-reaction exists between anti-H12 serum and the H1 type strain and between anti-H1 serum and the H12 type strain [Ewing, W. H.: Edwards and Ewing's identification of the *Enterobacteriaceae.*, Elsevier Science Publishers, Amsterdam, The Netherlands, 1986]. Strain M2126 carrying pPR1920 (carrying a flagellin gene from the H1 type strain, Table 3A) agglutinates with anti-H1 serum when the antiserum is diluted to 1:100, but agglutinates only with undiluted anti-H12 serum and not at a 1:10 dilution (please note that the antisera we used have been diluted before reaching our hands). In contrast, strain M2126 carrying plasmid pPR1990 (carrying a flagellin gene from the H12 type strain, Table 3A) agglutinates with anti-H12 serum when the antiserum is diluted at 1:100, but agglutinates only with undiluted anti-H1 serum and not at a 1:10 dilution. Thus, we conclude that the flagellin genes we sequenced from type strains for H1 and H12 encode flagellins of H1 and H12 specificities respectively.

10.3. Flagellin gene coding for H16:

Strain P5560 carrying plasmid pPR1969 agglutinated with anti-H16 serum. pPR1969 carries a flagellin gene amplified from the H3 type strain. It has been shown that this H3 type strain is a biphasic strain which can express H3 and H16 specificities [Ratiner, Y. A. (1985) "Two genetic arrangements determining flagellar antigen specificities in two diphasic *E. coli* strains. FEMS Microbiol Lett 19: 317-323]. Thus, the H3 type strain has two flagellin genes coding for H3 and H16 specificities. We conclude that we have cloned and sequenced the H16 flagellin gene from this H3 type strain.

10.4 Flagellin gene coding for H4:

The flagellin genes obtained from type strains for H4 and H17 are nearly identical, with 4 a.a. difference in the gene products. Plasmid pPR1955 carries a flagellin

gene from the H4 type strain, and plasmid pPR1957 carries a flagellin gene from the H17 type strain. Strain P5560 carrying plasmid pPR1955 or plasmid pPR1957 agglutinated with anti-H4 serum, but not with anti-H17 serum. It has been shown that the type strain for H17 is a biphasic strain which can express H17 and H4 [Ratiner, Y. A. (1985) "Two genetic arrangements determining flagellar antigen specificities in two diphasic *E. coli* strains. FEMS Microbiol Lett 19: 317-323]. The flagellin gene obtained from type strain for H44 is also highly similar to that obtained from the H4 type strain, with 2 a.a. difference in the gene products. It has been shown that the H44 type strain has two complete flagellin genes, being H4 and H44 [Ratiner, Y. A. (1998) "New flagellin specifying genes in some *E. coli* strains" J. Bacteriol 180: 979-984]. Thus, we conclude that all the three flagellin genes (obtained from type strains for H4, H17 and H44, and sequenced) encode the H4 flagellin, and that the flagellin genes for H17 and H44 specificities have not yet been cloned.

10.5 Flagellin gene coding for H10:

The flagellin genes obtained from type strains for H10 and H50 are nearly identical, with 3 a.a. difference in the gene products. Strain P5560 carrying plasmid pPR1923 (which carries a flagellin gene from the H10 type strain) agglutinated with anti-H10 serum. We conclude that the sequence obtained from the H10 type strain encodes the H10 flagellin. It is not clear if the sequence obtained from the H50 type strain encodes H10 or H50 (see below section for H50).

10.6 Flagellin gene coding for H38:

The flagellin genes obtained from type strains for H38 and H55 are nearly identical, with only 1 a.a. difference in the gene products. Strain M2126 carrying plasmid pPR1984 (carrying the flagellin gene from the type strain H38) agglutinated with anti-H38 serum, but not with

anti-H55 serum. It also has been shown that the type strain for H55 has two complete flagellin genes coding for H55 and H38 specificities [Ratiner, Y. A. (1998) "New flagellin specifying genes in some *E. coli* strains" J. Bacteriol 180: 979-984]. Thus, we conclude that both cloned genes encode the H38 flagellin.

10.7 *Summary:*

Flagellin genes coding for 39 H antigens have been identified, being those for specificities H1, H2, H4, H5, H6, H7, H9, H10, H11, H12, H14, H15, H16, H18, H19, H20, H21, H23, H24, H26, H27, H28, H29, H30, H31, H32, H33, H34, H38, H39, H41, H42, H43, H45, H46, H49, H51, H52, and H56.

11. Comparison and alignment of the flagellin genes:

Programs Pileup [Devereux, J., Haeberli, P. and Smithies, O.: A comprehensive set of sequence analysis programs for the VAX. Nucl. Acids Res. 12 (1984) 387-395]and Multicomp [Reeves, P.R., Farnell, L. and Lan, R.: MULTICOMP: a program for preparing sequence data for phylogenetic analysis. CABIOS 10 (1994) 281-284] were used.

The previously published sequence of H1 (GenBank accession number L07387) was extracted from GenBank and used. Because we did not sequence H36 and H53 flagellin genes and we did not have the H16 type strain, we only compared 51 flagellin genes of H type strains and the *fliC* genes from the additional 10 H7 strains.

Among the H7 *fliC* genes, the percentage of DNA difference ranged from 0.0 to 2.39%. The flagellin genes from type strains for H40 and H8 are identical. Some others are nearly identical: H21 and H47 (1.5% difference), H12 and H1 (2.6% difference), H10 and H50 (0.3% difference), H38 and H55 (0.1% difference), H4, H44 and H17 are very similar, the pairwise difference ranging from 0.33% to 0.87%.

For the flagellin genes obtained from type strains for H4, H17 and H44, we have shown that all the three genes encode flagellin with the H4 specificity (see above). For the flagellin genes obtained from type strains fro H21 and H47, and H38 and H55, we have confirmed the specificities for one for each pair and have good reason to conclude that both genes of each pair encode the same H specificity (see above section), being that for H21 and H38 specificities respectively.

For the flagellin genes obtained from type strains for H10 and H50, we have confirmed that the one from the H10 type strain encodes H10 specificity. As these two genes are highly similar, we have presumed that they both encode H10 specificity.

In the cases where the flagellin gene from two type strains is near identical, we conclude that both genes code for flagellin of the same H specificity and that one or other strain has an additional locus which carries the functional gene, although the flagellin genes sequenced do not appear to be mutated.

We have shown by cloning and expression that the flagellin genes obtained from the H1 and H12 type strains encode H1 and H12 specificities respectively (see above section). The neucleotide difference between these two genes is higher at 2.6% (see above), but still within the normal range for variation within a gene in *E. coli*. The two antigens cross react, and this cross reaction must be due to the high level similarity of the flagellins encoded by these two genes.

As discussed above, genes encoding some H antigens have been shown to be located at loci other than *fliC*. H3, H36, H47, H53 have been shown to be at a locus called *flkA*, H44 and H55 at *fllA*, and H54 at *flmA* [Ratiner Y A (1998)"New flagellin-specifying genes in some *Escherichia coli* strains" J. Bacteriol. 180 979-984]. However, these strains may carry a *fliC* in addition to *flkA*, *fllA* or *flmA* [Ratiner Y A (1998)"New flagellin-specifying genes in some

Escherichia coli strains" J. Bacteriol. 180 979-984].

The flagellin gene encoding H48 was previously sequenced from *E. coli* strain K-12 [Kuwajima G, Asaka J, Fujiwara T, Node K and Kondo E "Nucleotide sequence of the hag gene encoding flagellin of *Escherichia coli*" J Bacteriol. 168 (1986) 1479-1483]. We have sequenced the *fliC* gene from the H48 type strain, and found that it is identical to that from K-12.

The H54 gene is known to be at *flmA* [Ratiner Y A (1998)"New flagellin-specifying genes in some *Escherichia coli* strains" J. Bacteriol. 180 979-984]
and the finding of a non-functional presumptive *fliC* locus in the H54 strain shows that it is present but not expressed. However, we have not amplified and sequenced the functional *flmA* gene of this strain.

Using the 43 unique sequences (being the 39 identified genes with confirmed specificities and the flagellin genes obtained from the H8 (or H40), H25, H37, and H48 type strains) and the sequences from the two non-functional flagellin genes (from H type strains H35 and H54)(see Table 3) we have been able to determine antigen specific primers for each of the H antigen specificities and thereby show that it is practicable to detect *E.coli* strains carrying specific H antigens without false positives from strains of other H types. There is no reason to expect that the addition of 11 sequences to the 43 unique sequences obtained will affect the general conclusion, as unlike previous reports, our study covers flagellin sequences for a substantial majority of known *E. coli* H antigen specificities.

Our study of 11 H7 genes from strains of eight different O antigens shows limited variation which was such that the variation within genes for H antigens does not affect the ability to select antigen specific primers. O:H combinations in general define a strain and as some of the strains thus defined were quite distant from each other in a study by Whittam [Whittam T S, wolfe M L,

Wachsmuth I K, Orskov I and Wilson R A "Clonal relationships among *Escherichia coli* strains that cause hemorrhagic colitis and infantile diarrhea" Infect. Immun. 61 (1993) 1619-1629] the variation we observe is thought to represent that generally present in H7 genes. We also obtained more than one sequences for flagellin genes for H specificities H4, H10, and H38, and again the level of variation within a given specificities is very low. However, there is a low possibility that primers chosen without knowledge of the variation within genes of each H specificity could fail to give positive results with some isolates due to chance choice of primers which cover a base or bases which contribute to this low level variation. The variation within the H7 genes is in the normal range for variation within a gene in *E. coli* and if this possibility did occur it would be easy to use an alternate primer pair. For example, if a first primer in a primer pair is unable to hybridise to a target region because of low level variation in that region, a positive result may be achieved by using a second primer in that pair together with a third primer, whether or not the third primer is specific for the flagellin gene. Where the third primer is not specific for the flagellin gene, the specificity of the primer pair derives from the specificity of the second primer. The observation that the overall level of variation within gene for a given H specificity is very low making it extremely unlikely that the regions covered by the two primers specific for H specificity would both have undergone change in the same strain.

There are 54 known H antigens for *E. coli* and of these there are 11 H antigen specificities for which we do not as yet have sequence. It will be easy to determine these sequences and determine primer pairs specific for these H antigens by comparing these sequences with the 45 obtained sequences (see Table 3), and also modify the primers selected for any H antigen for which we already

know the sequence in the unlikely event that there is a possibility of false positives with the primers selected.

The sequences for the remaining H antigens can be obtained in one of the following ways:

1. where we have two bands by PCR (H36 and H53 type strains), we purify each and sequence, and also clone each into a strain mutated in its *fliC* gene and determine the H antigen expressed by use of specific sera. In this way a specific sequence can be related to an H antigen specificity. The other band which represents an H antigen gene for a different specificity is expected to include a mutant gene or a gene similar to one of those for a known H specificity, but if not may represent a new specificity for which primer pairs could be selected. It may be difficult to obtain expression of flagellin genes when cloned *from E. coli* due to cloning together with regulatory sequences which prevent expression. This is easily avoided by cloning the major segment of the gene into a functioning *fliC* gene to replace the equivalent segment of that gene, using standard site directed mutagenesis to give suitable restriction sites within the cloned gene and incorporating those restriction sites into primers used to amplify the major segment of the gene to be studied to facilitate the cloning. We have cloned and sequenced the PCR bands from the H36 and the H55 type strains using this method (see section 16).

2. Where two or more strains have the same flagellin gene sequence, the genes are cloned as above and the H antigen specificity represented by this sequence is determined. This identifies the strain in which the expected gene is expressed and also those strains for which we have sequenced a gene which is not being expressed. We then clone the gene for the antigen expressed in these strains by making a bank of plasmid clones using chromosomal DNA and select for a clone which

is expressing an H antigen different from the one represented by the known sequence. This can be done by taking advantage of the fact that the H antigen is on flagellin, the protein of the bacterial flagellum used for movement of the bacteria. In the presence of antibodies specific to that flagellum the bacteria cannot swim. For selection the clones are placed in a situation in which motile cells can swim away from the others and be collected. There are many versions of these techniques and any could be used. One version is to place the bacteria on a nutrient agar plate with reduced agar content such that bacteria can swim away from the site of inoculation. This is easily seen as growth on the plate and a sample of the bacteria which are motile can be recovered and cultivated. In this way bacteria carrying cloned H antigen genes can be selected. If the medium in the plate has antibody added to it only bacteria which express an H antigen different to that recognised by the antiserum will be able to swim. Specifically if the antiserum used is specific for the H antigen expressed by the gene for which we have sequence, only clones which express a different H antigen, such as those expressing the H antigen expressed by the H type strains used to make the plasmid, will be selected. Once the clone is obtained, the H antigen gene can be sequenced.

Our work has shown that there are at least 7 cases where the H antigen type strains carry two H antigen genes which appear to be complete and have the potential to function. However, while *E. coli* does not (in general) have a capacity to express more than one flagellin gene, it is striking that there are several loci for flagellin genes [Ratiner Y A (1998)"New flagellin-specifying genes in some *Escherichia coli* strains" J. Bacteriol. 180 979-984]. Several of the pairs of H type strains with identical or near identical sequence do not include any of the H antigen types shown by Ratiner [Ratiner Y A

(1998)"New flagellin-specifying genes in some *Escherichia coli* strains" J. Bacteriol. 180 979-984] to map other than at *fliC* although these predominate. This suggests that there are additional cases where the expressed gene is not the only flagellin gene present. However the fact that many of the cases where we obtained flagellin genes of identical or near identical sequence and/or two flagellin genes from one strain involve type strains found by Ratiner [Ratiner Y A (1998)"New flagellin-specifying genes in some *Escherichia coli* strains" J. Bacteriol. 180 979-984] to map away from *fliC* are among those near identical to others, indicates that the phenomenon is of limited extent. Nonetheless it remains possible even where only one gene has been obtained by PCR, that it is one of a pair of flagellin genes, the other not being amplified by the primers used, and further that it is the one not amplified which is expressing the H antigen of the strain. It will therefore be necessary to clone as described above each of the flagellin genes we have sequenced and confirm that it expresses the expected antigen to ensure that the invention give results corresponding to those of the traditional serotyping scheme. In the event that it does not, the gene for the type antigen can be cloned and sequenced by the means described above.

The 11 H7 *fliC* sequences fell into three groups, one comprising the genes from the O157:H7 and O55:H7 strains, which were identical, as expected given the proposed relationship between the clones. It has been shown that *E. coli* O157:H7 and O55:H7 clones are closely related [Whittam T S, wolfe M L, Wachsmuth I K, Orskov I and Wilson R A "Clonal relationships among *Escherichia coli* strains that cause hemorrhagic colitis and infantile diarrhea" Infect. Immun. 61 (1993) 1619-1629] thus it was expected that the H7 *fliC* genes from O157 and O55 would be identical. Among the H7 *fliC* sequences, we can identify primers specific to the H7 *fliC* gene for each of the three H7 groups. Two of these primers in combination with an H7

specific primer gave two primer pairs specific for the H7 gene of from the O157:H7 and O55:H7 clones.

13. Specific oligonucleotide primers for each of the 43 flagellin genes

Two oligonucleotide primers were chosen based on each of the 43 sequences. None of them had more than 85% identity with any other of 61 flagellin gene sequences. Thus, these primers are specific for each H type. These primers are listed in Table 3.

The flagellin gene of the H54 type strain is a mutated gene. It has an insertion sequence (IS1222) inserted into a normal flagellin gene of H21. Thus, primers for H21 would amplify a fragment of different size in H54. We also provide 2 primers based on the insertion sequence (see H54 row in Table 3), and the use of one of them in combination with one of the H21 primers will generate a PCR band only in H54, which will also differentiate those strain carrying the mutated H21 gene from those expressing the H21 flagellin gene.

The *flic* gene of H35 type strain is also a mutated gene. It has an insertion sequence (IS1) inserted into a normal flagellin gene of H11. Thus, primers for H11 would amplify a fragment of different size in H35. We also provide 2 primers based on the insertion sequence (see H35 row in Table 3), and the use of one of them in combination with one of the H11 primers will generate a PCR band only in H35, which will also differentiate those strain carrying the mutated H11 gene from those expressing the H11 flagellin gene.

14. Testing of the H7 specific oligonucleotide primers

Primer pair #1806/#1809 (see Table 3) was used to carry out PCR on chromosomal DNA samples of all the 54 H type strains and the H7 strains listed in Table 1. PCR reactions were carried out under the following conditions: denaturing, 94°C/30'; annealing, 58°C/30'; extension,

72°C/1'; 30 cycles. PCR reaction was carried out in an volume of 50ul for each of the chromosomal sample. After the PCR reaction, 5µl PCR product from each sample was run on an agarose gel to check for amplified DNA.

Primer pairs #1806/#1809 produced a band of predicted size with all the 11 strains expressing H7, but gave no band with other H type strains. Thus, these primers are H7 specific.

15. Testing of oligonucleotide primers specific to H7 of O157 and O55:

Based on a comparison of the *fliC* sequences of 11 different H7 strains, we have identified two oligonucleotides [#1696 (5'-GGCCTGACTCAGGCGGCC) at positions 178 to 195 in M527 and #1697 (5'-GAGTTACCGGCCTGCTGA) positions 1700-1683 in M527] which are unique to H7 of O157 and O55. Although not identical to any parts of the *fliC* sequences of any other H7 strains, these two primers are identical or have high level similarity to *fliC* genes of some other H types. However a combination of one of these primers with one of the H7 specific primers can give specificity for H7 of O157:H7 and O55:H7 *E. coli*.

Primer pairs #1696/#1809 and #1697/#1806 were used to carry out PCR on chromosomal DNA samples of all the H type strains and the H7 strains listed in Table 1. PCR reactions were carried out under the following conditions: denaturing, 94°C/30'; annealing, 61°C/30' (for #1696/#1809) or 60°C/30'(for#1697/#1806); extension, 72°C/1'; 30 cycles. PCR reaction was carried out in an volume of 50µl for each of the chromosomal samples. After the PCR reaction, 5µl PCR product from each sample was run on an agarose gel to check for amplified DNA.

Both primer pairs produced a band of predicted size with both of the O157:H7 strains (strains M1004 and M527, see Table 1), and the O55:H7 strain (strain M1686, see Table 1), but gave no band with other strains. Thus, these

two pairs of primers are specific to H7 genes of O157:H7 and O55:H7 *E. coli* strains.

16. Identification of flagellin genes for the remaining 15 H specificities.

16.1. Sequencing the potential flkA gene coding for the H36 flagellin:

Using primers #1431 (5'- atg gca caa gtc att aat acc caa c) and #1432 (5'- cta acc ctg cag cag aga ca), we have amplified two bands from the H36 type strain. PCR reaction was carried out under the following conditions: denaturing, 94oC/30'; annealing, 57oC/30'; extension, 72oC/1'; 30 cycles. These two PCR fragments were then cloned into the pGEM-T vector using the Promega pGEM-T cloning kit (Madison WI USA) to make plasmids pPR1992 and pPR1993. Inserts from both plasmids were first sequenced using the M13 universal primers (which bind to the pGEM-T DNA flanking the insertion site). For pPR1992, primers based on the sequence obtained were then used to sequence further, and this procedure was repeated until the insert was fully sequenced.

The sequence of the insert of pPR1992 is identical to that of the H12 flagellin gene sequence except perhaps for the first 8 and last 7 codons which are encoded by the PCR primers in plasmid pPR1992. We have only sequenced the two ends of the insert of plasmid pPR1993 (Figures 71 and 72), and the sequences of the two ends of the insert of pPR1993 are very similar to ends of other sequenced flagellin genes. We conclude that the insert of plasmid pPR1993 encodes a flagellin gene. The full sequence of the insert of plasmid pPR1993 can be obtained using the same method as for the sequencing of the insert of plasmid pPR1992. It is known that *flkA* gene encodes the H36 flagellin [Ratiner, Y. A. (1998) "New flagellin specifying genes in some *E. coli* strains" J. Bacteriol 180: 979-984], and it is highly likely that plasmid pPR1993 contains the

flkA gene of the H36 type strain. H specificities can be confirmed by slide agglutination.

The currently uncharacterised sequence of both ends and of DNA flanking these two sequenced genes can be obtained by PCR walking and sequencing. Methods for PCR walking from a known sequence to an unknown region in chromosomal DNA are available (see [Siebert, P. D. , A. Chenchi, D. E. Kellogg, A. Lukyanov and S. A. Lukyanov (1995) "An improved PCR method for walking in uncloned genomic DNA." Nuc. Acids Res. 23: 1087-1088]).

The sequenced genes then can be PCR amplified and cloned using the method(s) described in section 9. Flagellins expressed by strain M2126 carrying these plasmids then can be determined by use of specific sera.

The sequences flanking the *flkA* gene can then be used to PCR amplify other *flkA* genes (see below).

16.2 The flkA genes coding for H3, H47 and H53:

It has been shown that flagellins H3, H47 and H53 are encoded by *flkA* genes in the type strains [Ratiner, Y. A. (1998) "New flagellin specifying genes in some *E. coli* strains" J. Bacteriol 180: 979-984]. These genes can be PCR amplified using primers based on the sequences flanking the *flkA* gene in the H36 type strain. These PCR fragments can then be sequenced, and the genes expressed in strain M2126 for the identification of these genes.

16.3 The fllA genes coding for H44 and H55:

It is known that flagellins H44 and H55 are coded by *fllA* genes.

16.3.1 The H55 flagellin gene:

Using primers #1868 and #1870 (Table 3B), we have amplified two bands from the H55 type strain. PCR reaction was carried out under the following conditions: denaturing, 94oC/30'; annealing, 50oC/30'; extension, 72oC/1'; 30 cycles. These two PCR fragments were then

cloned into the pGEM-T vector using the Promega pGEM-T cloning kit (Madison WI USA) to make plasmids pPR1994 and pPR1989. Inserts from both plasmids were first sequenced using the M13 universal primers (which bind to the pGEM-T DNA flanking the insertion site). Primers based on the sequence obtained were then used to sequence further, and this procedure was repeated until both inserts were fully or partly sequenced.

The sequence of the insert of pPR1994 is highly similar to that of the flagellin gene of the H38 type strain, with 1 amino acid difference in the gene products. We have only sequenced the two ends of the insert of plasmid pPR1989 (figures 70A and 70B), and the sequences of the two ends of the insert of pPR1989 are very similar to ends of other sequenced flagellin genes. We conclude that the insert of plasmid pPR1989 encodes a flagellin gene. The full sequence of the insert of plasmid pPR1989 can be obtained using the same method as for the sequencing of the insert of plasmid pPR1994. It is known that the H55 type strain carries flagellin genes for both H38 and H55, and that the H55 flagellin gene is at the *fllA* locus [Ratiner, Y. A. (1998) "New flagellin specifying genes in some *E. coli* strains" J. Bacteriol 180: 979-984]. Thus, it is highly likely that plasmid pPR1989 contains the *fllA* gene of the H55 type strain.

The currently uncharacterised sequence of both ends and of DNA flanking these two sequenced genes can be obtained by PCR walking and sequencing. Methods for PCR walking from a known sequence to an unknown region in chromosomal DNA are available (see [Siebert, P. D. , A. Chenchi, D. E. Kellogg, A. Lukyanov and S. A. Lukyanov (1995) "An improved PCR method for walking in uncloned genomic DNA." Nuc. Acids Res. 23: 1087-1088]).

The sequenced genes then can be PCR amplified and cloned using the method(s) described in section 9. Flagellins expressed by strain M2126 carrying these plasmids then can be determined by use of specific sera.

16.3.2 The H44 flagellin gene:

The sequence information for DNA flanking the *fllA* gene in the H55 type strain can then be used to PCR, sequence and identify the *fllA* gene in the H44 type strain.

16.4 The flmA gene coding for H54:

This gene can be cloned by making a bank of plasmid clones in strain M2126 using chromosomal DNA of the H54 type strain and selecting for a transformant which is motile on an agar plate. This is done by taking advantage of the fact that the H antigen is on flagellin, the protein of the bacterial flagellum used for movement of the bacteria. Strain M2126 lacks flagellin. Once the clone(s) is obtained and identified by use of anti-H54 serum, the flagellin gene can be sequenced. It is possible that clones expressing different flagellin specificities can be obtained, and each of them can be identified by using different sera.

16.5 The flagellin genes obtained from the H37 and H48 type strains:

We have used primers #1868 and #1869 (both were based on the sequence obtained from the H48 type strain, also see section 9) and primers #1868 and #1870 (both were based on the sequences of the H7 flagellin gene of the H7 type strain, also see section 9) to PCR amplify and clone the sequenced flagellin genes from the H48 and H37 type strains respectively. Strain P5560 carrying the plasmid containing either the cloned gene was not motile and did not react with the appropriate antisera. It is highly likely that mutaions have occured due to PCR errors. This can be resolved by re-amplification and re-cloning of the genes.

16.6 The flagellin gene obtained from the H25 type

strain:

The flagellin gene sequence we first obtained from the H25 type strain lacks 23 and 21 codons at 5' and 3' ends respectively. We could not amplify the full gene from the H25 type strain using primers based on the H7 flagellin gene of the H7 type strain, and it was necessary to get the full sequence of this flagellin gene by other means.

We have used primers (#2650: 5' - cag cga tga aat act tgc cat and #2648: 5' - caa tgc ttc gtg acg cac) based on the genes (*fliD* and *fliA* respectively) flanking *fliC* gene in *E. coli* K-12 [Blattner, F. R., G. I. Plunkett, C. A. Bloch, N. T. Perna, V. Burland, M. Riley and et al. (1997) "The complete genome sequence of E. Coli Ki12" Science 277: 1453-1474] and primers (#2658: 5' - gcc tga gtc aga cct ttg and # 2653 5' - aac ctg tct gaa gcg cag) based on the flagellin sequence obtained from the H25 type strain to PCR amplify both ends of the flagellin gene. The PCR product was then sequenced, and we have now obtained the full flagellin gene sequence and sequence for the DNA flanking the flagellin gene from type strain H25 (Figure 69). Now, it is straightforward to PCR amplify, clone and express, and identify this gene using the methods described in sections 9 and 10.

16.7 The flagellin genes obtained from the H8 and H40 type strains:

The flagellin gene sequences obtained from both the H8 and H40 type strains lack 18 and 15 codons at 5' and 3' ends respectively. We have used primers based on the H7 flagellin gene of the H7 type strain to PCR amplify and clone the full genes from these two strains. Strain M2126 carrying plasmid made this way was not motile under microscope and did not react with the appropriate antisera. This could be due to PCR errors as mentioned in section 16.5 or perhaps the first and last few amino acids encoded by the primers (based on H7 flagellin gene) are

uncompatible in this case.

The full sequence of the full gene can be obtained using method described in section 16.6. The flagellin gene can then be PCR amplified, cloned and expressed, and identified using the methods described in sections 9 and 10.

The gene products of the flagellin genes obtained from the H8 and H40 type strains are identical. Thus, one of these two H specificities must be encoded by a unknown gene, and it can be cloned and identified using the method described in the section 16.8.

16.8 Flagellin genes coding for H17, H35, and H50:

As mentioned above, the sequenced flagellin genes from the H17 and H50 type strains encode H4 and H10 specificities respectively. The flagellin gene sequence obtained from the H35 strain has a insertion and encodes a non-functional gene (see section 8). Thus, genes coding for these flagellins have not been identified, and their location is unknown. One can use primers based on DNA flanking *fliC*, *fllA*, *flkA*, and *flmA* to do PCR on the type strain for each of the flagellin antigen. PCR products can then be sequenced, and possible genes can be cloned, expressed and identified then.

If the target gene is not PCR amplified using primers based on sequence of these loci or sequence flanking these loci, it can be cloned by making a bank of plasmid clones in strain M2126 using chromosomal DNA of the type strain and selecting for a transformant which is motile on an agar plate. This is done by taking advantage of the fact that the H antigen is on flagellin, the protein of the bacterial flagellum used for movement of the bacteria. Strain M2126 lacks flagellin. Once the clone(s) is obtained and identified by use of antisera, the flagellin gene can be sequenced. It is possible that clones expressing different flagellin antigens can be obtained,

and each of them can be identified by using different antisera. Antiserum for H50 can be prepared using standard methods [Ewing, W.H.:Edwards and Ewing's identification of the *Enterobacteriaceae*., Elsevier Science Publishers, Amsterdam, The Netherlands, 1986].

O antigen

Materials and Methods-part 1

The experimental procedures for the isolation and characterisation of the *E. coli* O111 O antigen gene cluster (position 3,021-9,981) are according to Bastin D.A., *et al.* 1991 "Molecular cloning and expression in *Escherichia coli* K-12 of the *rfb* gene cluster determining the O antigen of an *E. coli* O111 strain". *Mol. Microbiol.* 5:9 2223-2231 and Bastin D.A. and Reeves, P.R. 1995 "Sequence and analysis of the O antigen gene(*rfb*)cluster of *Escherichia coli* O111". *Gene* 164: 17-23.

A. Bacterial strains and growth media

Bacteria were grown in Luria broth supplemented as required.

B. Cosmids and phage

Cosmids in the host strain x2819 were repackaged *in vivo*. Cells were grown in 250mL flasks containing 30mL of culture, with moderate shaking at 30°C to an optical density of 0.3 at 580 nm. The defective lambda prophage was induced by heating in a water bath at 45°C for 15min followed by an incubation at 37°C with vigorous shaking for 2hr. Cells were then lysed by the addition of 0.3mL chloroform and shaking for a further 10min. Cell debris were removed from 1mL of lysate by a 5min spin in a microcentrifuge, and the supernatant removed to a fresh microfuge tube. One drop of chloroform was added then shaken vigorously through the tube contents.

C. DNA preparation

Chromosomal DNA was prepared from bacteria grown overnight at 37°C in a volume of 30mL of Luria broth. After harvesting by centrifugation, cells were washed and

resuspended in 10mL of 50mMTris-HCl pH 8.0. EDTA was added and the mixture incubated for 20min. Then lysozyme was added and incubation continued for a further 10min. Proteinase K, SDS, and ribonuclease were then added and the mixture incubated for up to 2hr for lysis to occur. All incubations were at 37°C. The mixture was then heated to 65°C and extracted once with 8mL of phenol at the same temperature. The mixture was extracted once with 5mL of phenol/chloroform/iso-amyl alcohol at 4°C. Residual phenol was removed by two ether extractions. DNA was precipitated with 2 vols. of ethanol at 4°C, spooled and washed in 70% ethanol, resuspended in 1-2mL of TE and dialysed. Plasmid and cosmid DNA was prepared by a modification of the Birnboim and Doly method [Birnboim, H. C. and Doly, J. (1979) "A rapid alkaline extraction procedure for screening recombinant plasmid DNA" *Nucl. Acid Res.* 7:1513-1523]. The volume of culture was 10mL and the lysate was extracted with phenol/chloroform/iso-amyl alcohol before precipitation with isopropanol. Plasmid DNA to be used as vector was isolated on a continuous caesium chloride gradient following alkaline lysis of cells grown in 1L of culture.

D. Enzymes and buffers.

Restriction endonucleases and DNA T4 ligase were purchased from Boehringer Mannheim (Castle Hill, NSW, Australia)or Pharmacia LKB (Melbourne, VIC Australia). Restriction enzymes were used in the recommended commercial buffer.

E. Construction of a gene bank.

Individual aliquots of M92 chromosomal DNA (strain Stoke W, from Statens Serum Institut, 5 Artillerivej, 2300 Copenhagen S, Denmark) were partially digested with 0.2U *Sau*3A1 for 1-15mins. Aliquots giving the greatest proportion of fragments in the size range of approximately 40-50kb were selected and ligated to vector pPR691 previously digested with *Bam*H1 and *Pvu*II. Ligation mixtures were packaged *in vitro* with packaging extract.

The host strain for transduction was x2819 and recombinants were selected with kanamycin.

F. Serological procedures.

Colonies were screened for the presence of the O111 antigen by immunoblotting. Colonies were grown overnight, up to 100 per plate then transferred to nitrocellulose discs and lysed with 0.5N HCl. Tween 20 was added to TBS at 0.05% final concentration for blocking, incubating and washing steps. Primary antibody was *E. coli* O group 111 antiserum, diluted 1:800. The secondary antibody was goat anti-rabbit IgG labelled with horseradish peroxidase diluted 1:5000. The staining substrate was 4-chloro-1-napthol. Slide agglutination was performed according to the standard procedure.

G. Recombinant DNA methods.

Restriction mapping was based on a combination of standard methods including single and double digests and sub-cloning. Deletion derivatives of entire cosmids were produced as follows: aliquots of 1.8mg of cosmid DNA were digested in a volume of 20ml with 0.25U of restriction enzyme for 5-80min. One half of each aliquot was used to check the degree of digestion on an agarose gel. The sample which appeared to give a representative range of fragments was ligated at 4°C overnight and transformed by the $CaCl_2$ method into JM109. Selected plasmids were transformed into sf174 by the same method. P4657 was transformed with pPR1244 by electroporation.

H. DNA hybridisation

Probe DNA was extracted from agarose gels by electroelution and was nick-translated using [a-32P]-dCTP. Chromosomal or plasmid DNA was electrophoresed in 0.8% agarose and transferred to a nitrocellulose membrane. The hybridisation and pre-hybridisation buffers contained either 30% or 50% formamide for low and high stringency probing respectively. Incubation temperatures were 42°C and 37°C for pre-hybridisation and hybridisation respectively. Low stringency washing of

filters consisted of 3 x 20min washes in 2 x SSC and 0.1% SDS. High-stringency washing consisted of 3 x 5min washes in 2 x SSC and 0.1% SDS at room temperature, a 1hr wash in 1 x SSC and 0.1% SDS at 58°C and 15min wash in 0.1 x SSC and 0.1% SDS at 58°C.

I. Nucleotide sequencing of *E. coli* O111 O antigen gene cluster (position 3,021-9,981)

Nucleotide sequencing was performed using an ABI 373 automated sequencer (CA, USA). The region between map positions 3.30 and 7.90 was sequenced using uni-directional exonuclease III digestion of deletion families made in PT7T3190 from clones pPR1270 and pPR1272. Gaps were filled largely by cloning of selected fragments into M13mp18 or M13mp19. The region from map positions 7.90-10.2 was sequenced from restriction fragments in M13mp18 or M13mp19. Remaining gaps in both the regions were filled by priming from synthetic oligonucleotides complementary to determined positions along the sequence, using a single stranded DNA template in M13 or phagemid. The oligonucleotides were designed after analysing the adjacent sequence. All sequencing was performed by the chain termination method. Sequences were aligned using SAP [Staden, R., 1982 "Automation of the computer handling of gel reading data produced by the shotgun method of DNA sequencing". *Nuc. Acid Res.* 10: 4731-4751; Staden, R., 1986 "The current status and portability of our sequence handling software". *Nuc. Acid Res.* 14: 217-231]. The program NIP [Staden, R. 1982 "An interactive graphics program for comparing and aligning nucleic acid and amino acid sequence". *Nuc. Acid Res.* 10: 2951-2961] was used to find open reading frames and translate them into proteins.

J. Isolation of clones carrying *E. coli* O111 O antigen gene cluster

The *E. coli* O antigen gene cluster was isolated according to the method of Bastin D.A., *et al.* [1991 "Molecular cloning and expression in Escherichia coli K-

12 of the *rfb* gene cluster determining the O antigen of an *E. coli* O111 strain". *Mol. Microbiol.* 5(9), 2223-2231]. Cosmid gene banks of M92 chromosomal DNA were established in the *in vivo* packaging strain x2819. From the genomic bank, 3.3 x 10^3 colonies were screened with *E.coli* O111 antiserum using an immuno-blotting procedure: 5 colonies (pPR1054, pPR1055, pPR1056, pPR1058 and pPR1287) were positive. The cosmids from these strains were packaged *in vivo* into lambda particles and transduced into the *E. coli* deletion mutant Sf174 which lacks all O antigen genes. In this host strain, all plasmids gave positive agglutination with O111 antiserum. An *Eco* R1 restriction map of the 5 independent cosmids showed that they have a region of approximately 11.5 kb in common (Figure 1). Cosmid pPR1058 included sufficient flanking DNA to identify several chromosomal markers linked to O antigen gene cluster and was selected for analysis of the O antigen gene cluster region.

K. Restriction mapping of cosmid pPR1058

Cosmid pPR1058 was mapped in two stages. A preliminary map was constructed first, and then the region between map positions 0.00 and 23.10 was mapped in detail, since it was shown to be sufficient for O111 antigen expression. Restriction sites for both stages are shown in Figure 2. The region common to the five cosmid clones was between map positions 1.35 and 12.95 of pPR1058.

To locate the O antigen gene cluster within pPR1058, pPR1058 cosmid was probed with DNA probes covering O antigen gene cluster flanking regions from *S. enterica* LT2 and *E.coli* K-12. Capsular polysaccharide (*cps*) genes lie upstream of O antigen gene cluster while the gluconate dehydrogenase (*gnd*) gene and the histidine (*his*) operon are downstream, the latter being further from the O antigen gene cluster. The probes used were pPR472 (3.35kb), carrying the *gnd* gene of LT2, pPR685 (5.3kb) carrying two genes of the *cps* cluster, *cpsB* and

cpsG of LT2, and K350 (16.5kb) carrying all of the *his* operon of K-12. Probes hybridised as follows: pPR472 hybridised to 1.55kb and 3.5 kb (including 2.7 kb of vector) fragments of *Pst*1 and *Hind*III double digests of pPR1246 (a *Hind*III/*Eco*R1 subclone derived from pPR1058, Figure 2), which could be located at map positions 12.95-15.1; pPR685 hybridised to a 4.4 kb *Eco*R1 fragment of pPR1058 (including 1.3 kb of vector) located at map position 0.00-3.05; and K350 hybridised with a 32kb *Eco*R1 fragment of pPR1058 (including 4.0kb of vector), located at map position 17.30-45.90. Subclones containing the presumed *gnd* region complemented a *gnd⁻edd⁻* strain GB23152. On gluconate bromothymol blue plates, pPR1244 and pPR1292 in this host strain gave the green colonies expected of a *gnd⁺edd⁻* genotype. The *his⁺* phenotype was restored by plasmid pPR1058 in the *his* deletion strain Sf174 on minimal medium plates, showing that the plasmid carries the entire his operon.

It is likely that the O antigen gene cluster region lies between *gnd* and *cps*, as in other *E. coli* and *S. enterica* strains, and hence between the approximate map positions 3.05 and 12.95. To confirm this, deletion derivatives of pPR1058 were made as follows: first, pPR1058 was partially digested with *Hind*III and self ligated. Transformants were selected for kanamycin resistance and screened for expression of O111 antigen. Two colonies gave a positive reaction. *Eco*R1 digestion showed that the two colonies hosted identical plasmids, one of which was designated pPR1230, with an insert which extended from map positions 0.00 to 23.10. Second pPR1058 was digested with *Sal*1 and partially digested with *Xho*1 and the compatible ends were re-ligated. Transformants were selected with kanamycin and screened for O111 antigen expression. Plasmid DNA of 8 positively reacting clones was checked using *Eco*R1 and *Xho*1 digestion and appeared to be identical. The cosmid of one was designated pPR1231. The insert of pPR1231

contained the DNA region between map positions 0.00 and 15.10. Third, pPR1231 was partially digested with *Xho*1, self-ligated, and transformants selected on spectinomycin/ streptomycin plates. Clones were screened for kanamycin sensitivity and of 10 selected, all had the DNA region from the *Xho*1 site in the vector to the *Xho*1 site at position 4.00 deleted. These clones did not express the O111 antigen, showing that the *Xho*1 site at position 4.00 is within the O antigen gene cluster. One clone was selected and named pPR1288. Plasmids pPR1230, pPR1231, and pPR1288 are shown in Figure 2.

L. Analysis of the *__E__. __coli__* *O111 O antigen gene cluster (position 3,021-9,981) nucleotide sequence data*

Bastin and Reeves [1995 "Sequence and analysis of the O antigen gene(*rfb*)cluster of *Escherichia coli* O111". *Gene* 164: 17-23] partially characterised the *E.coli* O111 O antigen gene cluster by sequencing a fragment from map position 3,021-9,981. Figure 3 shows the gene organisation of position 3,021-9,981 of *E. coli* O111 O antigen gene cluster. *orf3* and *orf6* have high level amino acid identity with *wcaH* and *wcaG* (46.3% and 37.2% respectively), and are likely to be similar in function to sugar biosynthetic pathway genes in the *E. coli* K-12 colanic gene cluster. *orf4* and *orf5* show high levels of amino acid homology to *manC* and *manB* genes respectively. *orf7* shows high level homology with *rfbH* which is an abequose pathway gene. *orf8* encodes a protein with 12 transmembrane segments and has similarity in secondary structure to other *wzx* genes and is likely therefore to be the O antigen flippase gene.

Materials and Methods-part 2

A. Nucleotide sequencing of 1 to 3,020 and 9,982 to 14,516 of the *E. coli* O111 O antigen gene cluster

The sub clones which contained novel nucleotide sequences, pPR1231 (map position 0 and 1,510), pPR1237 (map position -300 to 2,744), pPR1239 (map position 2,744

to 4,168), pPR1245 (map position 9,736 to 12,007) and pPR1246 (map position 12,007 to 15,300) (Figure 2), were characterised as follows: the distal ends of the inserts of pPR1237, pPR1239 and pPR1245 were sequenced using the M13 forward and reverse primers located in the vector. PCR walking was carried out to sequence further into each insert using primers based on the sequence data and the primers were tagged with M13 forward or reverse primer sequences for sequencing. This PCR walking procedure was repeated until the entire insert was sequenced. pPR1246 was characterised from position 12,007 to 14,516. The DNA of these sub clones was sequenced in both directions. The sequencing reactions were performed using the dideoxy termination method and thermocycling and reaction products were analysed using fluorescent dye and an ABI automated sequencer (CA, USA).

B. Analysis of the *E. coli* O111 O antigen gene cluster (positions 1 to 3,020 and 9,982 to 14,516 of Figure 5) nucleotide sequence data

The gene organisation of regions of *E. coli* O111 O antigen gene cluster which were not characterised by Bastin and Reeves [1995 "Sequence and analysis of the O antigen gene(*rfb*)cluster of *Escherichia coli* O111." *Gene* 164: 17-23],(positions 1 to 3,020 and 9,982 to 14,516) is shown in Figure 3. There are two open reading frames in region 1. Four open reading frames are predicted in region 2. The position of each gene is listed in Table 9.

The deduced amino acid sequence of *orf1* (*wbdH*) shares about 64% similarity with that of the *rfp* gene of *Shigella dysenteriae*. Rfp and WbdH have very similar hydrophobicity plots and both have a very convincing predicted transmembrane segment in a corresponding position. *rfp* is a galactosyl transferase involved in the synthesis of LPS core, thus *wbdH* is likely to be a galactosyl transferase gene. *orf2* has 85.7% identity at amino acid level to the *gmd* gene identified in the *E.*

coli K-12 colanic acid gene cluster and is likely to be a *gmd* gene. *orf9* encodes a protein with 10 predicted transmembrane segments and a large cytoplasmic loop. This inner membrane topology is a characteristic feature of all known 0 antigen polymerases thus it is likely that *orf9* encodes an 0 antigen polymerase gene, *wzy*. *orf10* (*wbdL*) has a deduced amino acid sequence with low homology with *Lsi2* of *Neisseria gonorrhoeae*. *Lsi2* is responsible for adding GlcNAc to galactose in the synthesis of lipooligosaccharide. Thus it is likely that *wbdL* is either a colitose or glucose transferase gene. *orf11* (*wbdM*) shares high level nucleotide and amino acid similarity with TrsE of *Yersinia enterocolitica*. TrsE is a putative sugar transferase thus it is likely that *wbdM* encodes the colitose or glucose transferase.

In summary three putative transferase genes and an 0 antigen polymerase gene were identified at map position 1 to 3,020 and 9,982 to 14,516 of *E. coli* O111 O antigen gene cluster. A search of GenBank has shown that there are no genes with significant similarity at the nucleotide sequence level for two of the three putative transferase genes or the polymerase gene. Figure 5 provides the nucleotide sequence of the O111 antigen gene cluster.

<u>Materials and Methods-part 3</u>

A. PCR amplification of O157 antigen gene cluster from an *E. coli* O157:H7 strain (Strain C664-1992, from Statens Serum Institut, 5 Artillerivej, 2300, Copenhagen S, Denmark)

E. coli O157 O antigen gene cluster was amplified by using long PCR [Cheng et al. 1994, "Effective amplification of long targets from cloned inserts and human and genomic DNA" P.N.A.S. USA 91: 5695-569] with one primer (primer #412: att ggt agc tgt aag cca agg gcg gta gcg t) based on the JumpStart sequence usually found in the promoter region of O antigen gene clusters [Hobbs,

et al. 1994 "The JumpStart sequence: a 39 bp element common to several polysaccharide gene clusters" Mol. Microbiol. 12: 855-856], and another primer #482 (cac tgc cat acc gac gac gcc gat ctg ttg ctt gg) based on the *gnd* gene usually found downstream of the O antigen gene cluster. Long PCR was carried out using the Expand Long Template PCR System from Boehringer Mannheim (Castle Hill NSW Australia), and products, 14 kb in length, from several reactions were combined and purified using the Promega Wizard PCR preps DNA purification System (Madison WI USA). The PCR product was then extracted with phenol and twice with ether, precipitated with 70% ethanol, and resuspended in 40mL of water.

B. Construction of a random DNase I bank:

Two aliquots containing about 150ng of DNA each were subjected to DNase I digestion using the Novagen DNase I Shotgun Cleavage (Madison WI USA) with a modified protocol as described. Each aliquot was diluted into 45ml of 0.05M Tris -HCl (pH7.5), 0.05mg/mL BSA and 10mM $MnCl_2$. 5mL of 1:3000 or 1:4500 dilution of DNaseI (Novagen) (Madison WI USA) in the same buffer was added into each tube respectively and 10ml of stop buffer (100mM EDTA), 30% glycerol, 0.5% Orange G, 0.075% xylene and cyanol (Novagen) (Madison WI USA) was added after incubation at 15°C for 5 min. The DNA from the two DNaseI reaction tubes were then combined and fractionated on a 0.8% LMT agarose gel, and the gel segment with DNA of about 1kb in size (about 1.5mL agarose) was excised. DNA was extracted from agarose using Promega Wizard PCR Preps DNA Purification (Madison WI USA) and resuspended in 200 mL water, before being extracted with phenol and twice with ether, and precipitated. The DNA was then resuspended in 17.25 mL water and subjected to T4 DNA polymerase repair and single dA tailing using the Novagen Single dA Tailing Kit (Madison WI USA). The reaction product (85ml containing about 8ng DNA) was then extracted with chloroform:isoamyl alcohol (24:1) once and

ligated to 3x 10^{-3} pmol pGEM-T (Promega) (Madison WI USA) in a total volume of 100mL. Ligation was carried out overnight at 4°C and the ligated DNA was precipitated and resuspended in 20mL water before being electroporated into *E. coli* strain JM109 and plated out on BCIG-IPTG plates to give a bank.

C. Sequencing

DNA templates from clones of the bank were prepared for sequencing using the 96-well format plasmid DNA miniprep kit from Advanced Genetic Technologies Corp (Gaithersburg MD USA) The inserts of these clones were sequenced from one or both ends using the standard M13 sequencing primer sites located in the pGEM-T vector. Sequencing was carried out on an ABI377 automated sequencer (CA USA) as described above, after carrying out the sequencing reaction on an ABI Catalyst (CA USA). Sequence gaps and areas of inadequate coverage were PCR amplified directly from O157 chromosomal DNA using primers based on the already obtained sequencing data and sequenced using the standard M13 sequencing primer sites attached to the PCR primers.

D. Analysis of the *E. coli* O157 O antigen gene cluster nucleotide sequence data

Sequence data were processed and analysed using the Staden programs [Staden, R., 1982 "Automation of the computer handling of gel reading data produced by the shotgun method of DNA sequencing." *Nuc. Acid Res.* 10: 4731-4751; Staden, R., 1986 "The current status and portability of our sequence handling software". *Nuc. Acid Res.* 14: 217-231; Staden, R. 1982 "An interactive graphics program for comparing and aligning nucleic acid and amino acid sequence". *Nuc. Acid Res.* 10: 2951-2961]. Figure 4 shows the structure of *E. coli* O157 O antigen gene cluster. Twelve open reading frames were predicted from the sequence data, and the nucleotide and amino acid sequences of all these genes were then used to search the GenBank database for indication of possible function and

specificity of these genes. The position of each gene is listed in Table 9. The nucleotide sequence is presented in Figure 6.

orfs 10 and 11 showed high level identity to *manC* and *manB* and were named *manC* and *manB respectively. orf7* showed 89% identity (at amino acid level) to the *gmd* gene of the *E. coli* colanic acid capsule gene cluster (Stevenson G., K. *et al.* 1996 "Organisation of the *Escherichia coli* K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid".J. Bacteriol. 178:4885-4893) and was named *gmd*. *orf8* showed 79% and 69% identity (at amino acid level) respectively to *wcaG* of the *E. coli* colanic acid capsule gene cluster and to *wbcJ* (*orf14.8*) gene of the *Yersinia enterocolitica* O8 O antigen gene cluster (Zhang, L. *et al.* 1997 "Molecular and chemical characterization of the lipopolysaccharide O-antigen and its role in the virulence of *Y. enterocolitica* serotype O8".Mol. Microbiol. 23:63-76). Colanic acid and the *Yersinia* O8 O antigen both contain fucose as does the O157 O antigen. There are two enzymatic steps required for GDP-L-fucose synthesis from GDP-4-keto-6-deoxy-D-mannose, the product of the *gmd* gene product. However, it has been shown recently (Tonetti, M *et al.* 1996 Synthesis of GDP-L-fucose by the human FX protein J. Biol. Chem. 271:27274-27279) that the human FX protein has "significant homology" with the *wcaG* gene (referred to as *Yefb* in that paper), and that the FX protein carries out both reactions to convert GDP-4-keto-6-deoxy-D-mannose to GDP-L-fucose. We believe that this makes a very strong case for *orf8* carrying out these two steps and propose to name the gene *fcl*. In support of the one enzyme carrying out both functions is the observation that there are no genes other than *manB*, *manC*, *gmd* and *fcl* with similar levels of similarity between the three bacterial gene clusters for fucose containing structures.

orf5 is very similar to *wbeE* (*rfbE*) of *Vibrio*

cholerae O1, which is thought to be the perosamine synthetase, which converts GDP-4-keto-6-deoxy-D-mannose to GDP-perosamine (Stroeher, U.H *et al.* 1995 "A putative pathway for perosamine biosynthesis is the first function encoded within the *rfb* region of *Vibrio cholerae*" O1. Gene 166: 33-42). *V. cholerae* O1 and *E. coli* O157 O antigens contain perosamine and N-acetyl-perosamine respectively. The *V. cholerae* O1 *manA*, *manB*, *gmd* and *wbeE* genes are the only genes of the *V. cholerae* O1 gene cluster with significant similarity to genes of the *E. coli* O157 gene cluster and we believe that our observations both confirm the prediction made for the function of *wbe* of *V. cholerae*, and show that *orf5* of the O157 gene cluster encodes GDP-perosamine synthetase. *orf5* is therefore named *per*. *orf5* plus about 100bp of the upstream region (postion 4022-5308)was previously sequenced by Bilge, S.S. *et al.* [1996 "Role of the *Escherichia coli* O157-H7 O side chain in adherence and analysis of an *rfb* locus".Infect. Immun. 64:4795-4801].

orf12 shows high level similarity to the conserved region of about 50 amino acids of various members of an acetyltransferase family (Lin, W., *et al.* 1994 "Sequence analysis and molecular characterisation of genes required for the biosynthesis of type 1 capsular polysaccharide in *Staphylococcus aureus*". J. Bateriol. 176: 7005-7016) and we believe it is the N-acetyltransferase to convert GDP-perosamine to GDP-perNAc. *orf12* has been named *wbdR*.

The genes *manB*, *manC*, *gmd*, *fcl*, *per* and *wbdR* account for all of the expected biosynthetic pathway genes of the O157 gene cluster.

The remaining biosynthetic step(s) required are for synthesis of UDP-GalNAc from UDP-Glc. It has been proposed (Zhang, L., *et al.* 1997 "Molecular and chemical characterisation of the lipopolysaccharide O-antigen and its role in the virulence of *Yersinia enterocolitica* serotype O8".Mol. Microbiol. 23:63-76) that in *Yersinia enterocolitica* UDP-GalNAc is synthesised from UDP-GlcNAc

by a homologue of galactose epimerase (GalE), for which there is a *galE* like gene in the *Yersinia enterocolitica* O8 gene cluster. In the case of O157 there is no *galE* homologue in the gene cluster and it is not clear how UDP-GalNAc is synthesised. It is possible that the galactose epimerase encoded by the *galE* gene in the *gal* operon, can carry out conversion of UDP-GlcNAc to UDP-GalNAc in addition to conversion of UDP-Glc to UDP-Gal. There do not appear to be any gene(s) responsible for UDP-GalNAc synthesis in the O157 gene cluster.

orf4 shows similarity to many *wzx* genes and is named *wzx* and *orf2* which shows similarity of secondary structure in the predicted protein to other *wzy* genes and is for that reason named *wzy*.

The *orf1*, *orf3* and *orf6* gene products all have characteristics of transferases, and have been named *wbdN*, *wbdO* and *wbdP* respectively. The O157 O antigen has 4 sugars and 4 transferases are expected. The first transferase to act would put a sugar phosphate onto undecaprenol phosphate. The two transferases known to perform this function, WbaP (RfbP) and WecA (Rfe) transfer galactose phosphate and N-acetyl-glucosamine phosphate respectively to undecaprenol phosphate. Neither of these sugars is present in the O157 structure.

Further, none of the presumptive transferases in the O157 gene cluster has the transmembrane segments found in *WecA* and WbaP which transfer a sugar phosphate to undecaprenol phosphate and expected for any protein which transferred a sugar to undecaprenol phosphate which is embedded within the membrane.

The *WecA* gene which transfers GlcNAc-P to undecaprenol phosphate is located in the Enterobactereal Common Antigen (ECA) gene cluster and it functions in ECA synthesis in most and perhaps all *E. coli* strains, and also in O antigen synthesis for those strains which have GlcNAc as the first sugar in the O unit.

It appears that WecA acts as the transferase for

addition of GalNAc-1-P to undecaprenol phosphate for the *Yersinia enterocolitica* O8 O antigen [Zhang et al.1997 "Molecular and chemical characterisation of the lipopolysaccharide O antigen and its role in the virulence of *Yersinia enterocolitica* serotype O8" Mol. Microbiol. 23: 63-76.] and perhaps does so here as the O157 structure includes GalNAc. *WecA* has also been reported to add Glucose-1-P phosphate to undecaprenol phosphate in *E. coli* O8 and O9 strains, and an alternative possibility for transfer of the first sugar to undecaprenol phosphate is *WecA* mediated transfer of glucose, as there is a glucose residue in the O157 O antigen. In either case the requisite number of transferase genes are present if GalNAc or Glc is transferred by *WecA* and the side chain Glc is transferred by a transferase outside of the O antigen gene cluster.

orf9 shows high level similarity (44% identity at amino acid level, same length) with *wcaH* gene of the *E. coli* colanic acid capsule gene cluster. The function of this gene is unknown, and we give *orf9* the name *wbdQ*.

The DNA between *manB* and *wdbR* has strong sequence similarity to one of the H-repeat units of *E. coli* K12. Both of the inverted repeat sequences flanking this region are still recognisable, each with two of the 11 bases being changed. The H-repeat associated protein encoding gene located within this region has a 267 base deletion and mutations in various positions. It seems that the H-repeat unit has been associated with this gene cluster for a long period of time since it translocated to the gene cluster, perhaps playing a role in assembly of the gene cluster as has been proposed in other cases.

Materials and Methods - part 4

To test our hypothesis that O antigen genes for transferases and the *wzx*, *wzy* genes were more specific than pathway genes for diagnostic PCR, we first carried out PCR using primers for all the *E. coli* O16 O antigen

genes (Table 7). The PCR was then carried out using PCR primers for *E.coli* O111 transferase, *wzx* and *wzy* genes (Table 8, 8A). PCR was also carried out using PCR primers for the *E. coli* O157 transferase, *wzx* and *wzy* genes (Table 9, 9A).

Chromosomal DNA from the 166 serotypes of *E. coli* available from Statens Serum Institut, 5 Artillerivej, 2300 Copenhagen Denmark was isolated using the Promega Genomic (Madison WI USA) isolation kit. Note that 164 of the serogroups are described by Ewing W. H.: Edwards and Ewings "Identification of the Enterobacteriacea" Elsevier, Amsterdam 1986 and that they are numbered 1-171 with numbers 31, 47, 67, 72, 93, 94 and 122 no longer valid. Of the two serogroup 19 strains we used 19ab strain F8188-41. Lior H. 1994 ["Classification of *Escherichia coli* In Escherichia coli in domestic animals and humans pp 31-72. Edited by C.L. Gyles CAB international] adds two more numbered 172 and 173 to give the 166 serogroups used. Pools containing 5 to 8 samples of DNA per pool were made. Pool numbers 1 to 19 (Table 4) were used in the *E. coli* O111 and O157 assay. Pool numbers 20 to 28 were also used in the O111 assay, and pool numbers 22 to 24 contained *E. coli* O111 DNA and were used as positive controls (Table 5). Pool numbers 29 to 42 were also used in the O157 assay, and pool numbers 31 to 36 contained *E. coli* O157 DNA, and were used as positive controls (Table 6). Pool numbers 2 to 20, 30, 43 and 44 were used in the *E. coli* O16 assay (Tables 4 to 6). Pool number 44 contained DNA of *E. coli* K-12 strains C600 and WG1 and was used as a positive control as between them they have all of the *E. coli* K-12 O16 O antigen genes.

PCR reactions were carried out under the following conditions: denaturing 94°C/30″; annealing, temperature varies (refer to Tables)/30″; extension, 72°C/1′; 30 cycles. PCR reaction was carried out in an volume of 25mL for each pool. After the PCR reaction, 10mL PCR

product from each pool was run on an agarose gel to check for amplified DNA.

Each *E. coli* chromosomal DNA sample was checked by gel electrophoresis for the presence of chromosomal DNA and by PCR amplification of the *E. coli mdh* gene using oligonucleotides based on *E. coli* K-12 [Boyd *et al.* (1994) "Molecular genetic basis of allelic polymorphism in malate degydrogenase (*mdh*) in natural populations of *Escherichia coli* and Salmonella enterica" Proc. Nat. Acad. Sci. USA. 91:1280-1284.] Chromosomal DNA samples from other bacteria were only checked by gel electrophoresis of chromosomal DNA.

A. Primers based on *E. coli* O16 O antigen gene cluster sequence.

The O antigen gene cluster of *E. coli* O16 was the only typical *E. coli* O antigen gene cluster that had been fully sequenced prior to that of O111, and we chose it for testing our hypothesis. One pair of primers for each gene was tested against pools 2 to 20, 30 and 43 of *E. coli* chromosomal DNA. The primers, annealing temperatures and functional information for each gene are listed in Table 8.

For the five pathway genes, there were 17/21, 13/21, 0/21, 0/21, 0/21 positive pools for *rmlB*, *rmlD*, *rmlA*, *rmlC* and *glf* respectively (Table 7). For the *wzx*, wzy and three transferase genes there were no positives amongst the 21 pools of *E. coli* chromosomal DNA tested (Table 7). In each case the #44 pool gave a positive result.

B. Primers based on the *E. coli* O111 O antigen gene cluster sequence.

One to four pairs of primers for each of the transferase, *wzx* and *wzy* genes of O111 were tested against the pools 1 to 21 of *E. coli* chromosomal DNA (Table 8). For *wbdH*, four pairs of primers, which bind

to various regions of this gene, were tested and found to be specific for O111 as there was no amplified DNA of the correct size in any of those 21 pools of *E. coli* chromosomal DNA tested. Three pairs of primers for *wbdM* were tested, and they are all specific although primers #985/#986 produced a band of the wrong size from one pool. Three pairs of primers for *wzx* were tested and they all were specific. Two pairs of primers were tested for *wzy*, both are specific although #980/#983 gave a band of the wrong size in all pools. One pair of primers for *wbdL* was tested and found unspecific and therefore no further test was carried out. Thus, *wzx, wzy* and two of the three transferase genes are highly specific to O111. Bands of the wrong size found in amplified DNA are assumed to be due to chance hybridisation of genes widely present in *E. coli*. The primers, annealing temperatures and positions for each gene are in Table 8.

The O111 assay was also performed using pools including DNA from O antigen expressing *Yersinia pseudotuberculosis*, *Shigella boydii* and *Salmonella enterica* strains (Table 8A). None of the oligonucleotides derived from *wbdH, wzx, wzy or wbdM* gave amplified DNA of the correct size with these pools. Notably, pool number 25 includes *S. enterica* Adelaide which has the same O antigen as *E. coli* O111: this pool did not give a positive PCR result for any primers tested indicating that these genes are highly specific for *E. coli* O111.

Each of the 12 pairs binding to *wbdH, wzx, wzy and wbdM* produces a band of predicted size with the pools containing O111 DNA (pools number 22 to 24). As pools 22 to 24 included DNA from all strains present in pool 21 plus O111 strain DNA (Table 5), we conclude that the 12 pairs of primers all give a positive PCR test with each of three unrelated O111 strains but not with any other strains tested. Thus these genes are highly specific for *E. coli* O111.

C. Primers based on the *E. coli* O157 O antigen gene cluster sequence.

Two or three primer pairs for each of the transferase, *wzx* and *wzy* genes of O157 were tested against *E. coli* chromosomal DNA of pools 1 to 19, 29 and 30 (Table 9). For *wbdN*, three pairs of primers, which bind to various regions of this gene, were tested and found to be specific for O157 as there was no amplified DNA in any of those 21 pools of *E. coli* chromosomal DNA tested. Three pairs of primers for *wbdO* were tested, and they are all specific although primers # 1211/#1212 produced two or three bands of the wrong size from all pools. Three pairs of primers were tested for *wbdP* and they all were specific. Two pairs of primers were tested for *wbdR* and they were all specific. For *wzy*, three pairs of primers were tested and all were specific although primer pair #1203/#1204 produced one or three bands of the wrong size in each pool. For *wzx*, two pairs of primers were tested and both were specific although primer pair #1217/#1218 produced 2 bands of wrong size in 2 pools, and 1 band of wrong size in 7 pools. Bands of the wrong size found in amplified DNA are assumed to be due to chance hybridisation of genes widely present in *E. coli*. The primers, annealing temperatures and function information for each gene are in Table 9.

The O157 assay was also performed using pools 37 to 42, including DNA from O antigen expressing *Yersinia pseudotuberculosis*, *Shigella boydii*, *Yersinia enterocolitica* O9, *Brucella abortus* and *Salmonella enterica* strains (Table 9A). None of the oligonucleotides derived from *wbdN*, *wzy*, *wbdO*, *wzx*, *wbdP* or *wbdR* reacted specifically with these pools, except that primer pair #1203/#1204 produced two bands with *Y. enterocolitica* O9 and one of the bands is of the same size with that from the positive control. Primer pair #1203/#1204 binds to *wzy*. The predicted secondary

structures of Wzy proteins are generally similar, although there is very low similarity at amino acid or DNA level among the sequenced *wzy* genes. Thus, it is possible that *Y. enterocolitica* O9 has a *wzy* gene closely related to that of *E. coli* O157. It is also possible that this band is due to chance hybridization of another gene, as the other two *wzy* primer pairs (#1205/#1206 and #1207/#1208) did not produce any band with *Y. enterocolitica* O9. Notably, pool number 37 includes *S. enterica* Landau which has the same O antigen as *E. coli* O157, and pool 38 and 39 contain DNA of *B. abortus* and *Y. enterocolitica* O9 which cross react serologically with *E. coli* O157. This result indicates that these genes are highly O157 specific, although one primer pair may have cross reacted with *Y. enterocolitica* O9.

Each of the 16 pairs binding to *wbdN, wzx, wzy, wbdO, wbdP* and *wbdR* produces a band of predicted size with the pools containing O157 DNA (pools number 31 to 36). As pool 29 included DNA from all strains present in pools 31 to 36 other than O157 strain DNA (Table 6), we conclude that the 16 pairs of primers all give a positive PCR test with each of the five unrelated O157 strains.

Thus PCR using primers based on genes *wbdN, wzy, wbdO, wzx, wbdP* and *wbdR* is highly specific for *E. coli* O157, giving positive results with each of six unrelated O157 strains while only one primer pair gave a band of the expected size with one of three strains with O antigens known to cross-react serologically with *E. coli* O157.

TABLE 1

H7 strains used in this work in addition to the H antigens type strains

Name used in this study	Serotype	Original name	Source*
M527	O157:H7	C664-1992	a
M917	O18ac:H7	A57	IMVS
M918	O18ac:H7	A62	IMVS
M973	O2:H7	A1107	CDC
M1004	O157:H7	EH7	b
M1179	O18ac:H7	D-M3291/54	IMVS
M1200	O7:H7	A64	c
M1211	O19ab:H7	F8188-41	IMVS
M1328	O53:H7	14097	IMVS
M1686	O55:H7	TB156	d

*

a. Statens Serum Institut, Copenhagen, Denmark.

b. Dr R. Brown of Royal Children's Hospital, Melbourne, Australia.

c. Max-Planck Institut fur molekulare Genetik, Berlin, Germany.

d. Dr P. Tarr of Children's Hospital and Medical Center, University of Washington, USA.

IMVS, Institute of Medical and veterinary Science, Adelaide, Australia.

CDC, Centers for Disease Control and prevention, Atlanta, USA.

Table 2

Oligonucleotides used to PCR amplify *fliC* genes from different H type strains for sequencing		
H Type Strains	Annealing Temperature (°C)	Primers Used
1	55	#1575/#1576
2	55	#1285/#1286
3	55	#1285/#1286
4	50	$1431/#1432
5	60	#1285/#1286
6	55	#1575/#1576
7	55	#1575/#1576
8	55	#1431/#1432
9	60	#1575/#1576
10	55	#1575/#1576
11	55	#1285/#1286
12	60	#1575/#1576
14	60	#1575/#1576
15	60	#1575/#1576
16	60	#1575/#1576
17	60	#1417/#1418
18	60	#1575/#1576
19	60	#1575/#1576
20	60	#1575/#1576
21	55	#1285/#1286
23	60	#1575/#1576
24	60	#1285/#1286
25	60	#1417/#1418
26	60	#1575/#1576
27	50	#1431/#1432
28	60	#1575/#1576
29	60	#1285/#1286
30	60	#1575/#1576
31	60	#1575/#1576
32	60	#1575/#1576
33	60	#1285/1286
34	55	#1575/#1576
35	50	#1431/#1432
37	60	#1285/#1286
38	60	#1285/#1286
39	55	#1285/#1286
40	55	#1285/#1286
41	60	#1575/#1576
42	60	#1285/#1286
43	60	#1575/#1576
44	60	#1285/#1286
45	60	#1575/#1576
46	60	#1575/#1576
47	55	#1285/#1286
48	60	#1575/#1576
49	60	#1575/#1576
50	60	#1285/#1286
51	60	#1575/#1576
52	60	#1575/#1576
54	50	#1431/#1432
55	60	#1285/#1286
56	60	#1285/#1286

Table 3
Summary of the flagellin sequences obtained and specific H type oligonucleotide primers

H type strain(s) the sequenced gene(s) obtained from	H specificity coded by the gene(s)	H type strain from which the flagellin gene sequence was used for primer choice	Positions of primer 1	Positions of primer 2
1	1	1	892-909	1172-1189
2	2	2	568-587	1039-1056
4,17,44	4	4	466-483	628-648
5	5	5	697-714	877-897
6	6	6	565-585	799-816
7	7	7	553-570 (primer #1806)	1483-1500 (primer #1809)
9	9	9	616-633	838-855
10(50)***	10	10	559-579	697-717
11	11	11	586-606*	791-810*
12	12	12	892-909	1172-1189
14	14	14	586-606	793-813
15	15	15	640-660	817-834
3	16	3	649-666	925-942
18	18	18	589-606	802-819
19	19	19	607-624	538-855
20	20	20	574-591	760-780
21,47	21	21	676-693**	862-879**
23	23	23	637-654	1336-1353
24	24	24	496-516	772-792
26	26	26	553-570	772-789
27	27	27	685-702	799-819
28	28	28	592-609	778-798
29	29	29	538-555	757-774
30	30	30	814-831	943-962
31	31	31	571-588	790-807
32	32	32	514-831	1057-1074
33	33	33	553-570	718-735
34	34	34	568-585	796-816
38,55	38	38	553-573	709-729
39	39	39	556-573	718-735
41	41	41	598-615	784-801
42	42	42	547-567	715-735
43	43	43	580-597	844-861
45	45	45	640-657	943-963
46	46	46	565-582	781-801
49	49	49	589-609	754-771
51	51	51	565-582	1042-1059
52	52	52	598-615	829-846
56	56	56	697-714	877-897
8 and 40		8	562-579	1045-1062
25		25	529-549	703-723
35		non-functional H11 gene	769-789*	1045-1065*
37		37	520-537	715-735
48		48	568-585	835-852
54		non-functional H21 gene	988-1008**	1344-1364**

* See section 13 for choice of primers for the flagellin gene of H11
** See section 13 for choice of primers for the flagellin gene of H21
*** See text

Table 3A

Cloning, expression and identification of flagellin genes

H type strain from which the H antigen gene was amplified	Primers used for PCR amplification of the H antigen gene	Annealing temperature (oC) used for PCR amplification	Plasmid carrying the H antigen gene	Host strain used for expression	Anti-serum which reacts with an *E. Coli fliC* deletion strain carrying the plasmid	H antigen encoded by the cloned gene
H1	#1868 & #1870	55	pPR1920	M2126	H1	H1
H2	#1868 & #1870	55	pPR1977	P5560	H2	H2
H3	#1868 & #1870	55	pPR1969	P5560	H16	H16
H4	#1878 & #1885	65	pPR1955	P5560	H4	H4
H5	#1868 & #1870	60	pPR1967	M2126	H5	H5
H6	#1868 & #1870	55	pPR1921	P5560	H6	H6
H7	#1868 & #1870	55	pPR1919	P5560	H7	H7
H9	#1868 & #1870	55	pPR1922	P5560	H9	H9
H10	#1868 & #1870	55	pPR1923	P5560	H10	H10
H11	#1868 & #1870	55	pPR1981	M2126	H11	H11
H12	#1868 & #1870	60	pPR1990	M2126	H12	H12
H14	#1868 & #1870	55	pPR1924	P5560	H14	H14
H15	#1868 & #1870	55	pPR1925	P5560	H15	H15
H17	#1878 & #1885	65	pPR1957	P5560	H4	H4
H18	#1868 & #1870	55	pPR1986	M2126	H18	H18
H19	#1868 & #1870	55	pPR1927	P5560	H19	H19
H20	#1868 & #1870	55	pPR1963	M2126	H20	H20
H21	#1868 & #1870	55	pPR1995	M2126	H21	H21
H23	#1868 & #1869	55	pPR1942	P5560	H23	H23
H24	#1868 & #1870	55	pPR1971	M2126	H24	H24
H26	#1868 & #1870	65	pPR1928	P5560	H26	H26
H27	#1868 & #1870	55	pPR1970	M2126	H27	H27
H28	#1868 & #1870	60	pPR1944	P5560	H28	H28
H29	#1868 & #1870	55	pPR1972	M2126	H29	H29
H30	#1868 & #1871	55	pPR1948	P5560	H30	H30
H31	#1868 & #1870	65	pPR1965	M2126	H31	H31
H32	#1868 & #1871	55	pPR1940	P5560	H32	H32
H33	#1868 & #1871	55	pPR1976	M2126	H33	H33
H34	#1868 & #1870	65	pPR1930	P5560	H34	H34
H38	#1868 & #1870	48	pPR1984	M2126	H38	H38
H39	#1868 & #1870	48	pPR1982	M2126	H39	H39
H41	#1868 & #1870	65	pPR1931	P5560	H41	H41
H42	#1868 & #1870	50	pPR1979	M2126	H42	H42
H43	#1868 & #1870	65	pPR1968	M2126	H43	H43
H45	#1868 & #1870	60	pPR1943	P5560	H45	H45
H46	#1868 & #1870	60	pPR1966	M2126	H46	H46
H49	#1868 & #1870	60	pPR1985	M2126	H49	H49
H51	#1868 & #1870	65	pPR1941	P5560	H51	H51
H52	#1868 & #1870	65	pPR1935	P5560	H52	H52
H56	#1868 & #1870	50	pPR1978	M2126	H56	H56

Table 3B Oligonucleotide primers used for PCR amplification and cloning of H antigen genes

#1868 5'- cat gcc atg gca caa gtc att aat acc -3'
*Nco*I

#1869 5'- ata tgt cga ctt aac cct gca gca gag aca g -3'
*Sal*I

#1870 5' - atg gat cct taa ccc tgc agc aga gac ag -3'
*Bam*HI

#1871 5' - aac tgc agt taa ccc tgt agc aga gac ag -3'
*Pst*I

#1872 5' - cgg gat ccc gca gac tgg ttc ttg ttg at - 3'
*Bam*HI

#1878 5' - cgg gat cca ctt cta tcg agc gcc tct ct - 3'
*Bam*HI

#1884 5' - gct cta gag cgc aga tca ttc agc agg cc -3'
*Xba*I

#1885 5' - gct cta gac atg ttg gac act tcg gtc gc - 3'
*Xba*I

TABLE 4

Pool No.	Strains of which chromosonal DNA included in the pool	Source*
1	*E. coli* type strains for O serotypes 1, 2, 3, 4, 10, 16, 18 and 39	IMVS[a]
2	*E. coli* type strains for O serotypes 40, 41, 48, 49, 71, 73, 88 and 100	IMVS
3	*E. coli* type strains for O serotypes 102, 109, 119, 120, 121, 125, 126 and 137	IMVS
4	*E. coli* type strains for O serotypes 138, 139, 149, 7, 5, 6, 11 and 12	IMVS
5	*E. coli* type strains for O serotypes 13, 14, 15, 17, 19ab, 20, 21 and 22	IMVS
6	*E. coli* type strains for O serotypes 23, 24, 25, 26, 27, 28, 29 and 30	IMVS
7	*E. coli* type strains for O serotypes 32, 33, 34, 35, 36, 37, 38 and 42	IMVS
8	*E. coli* type strains for O serotypes 43, 44, 45, 46, 50, 51, 52 and 53	IMVS
9	*E. coli* type strains for O serotypes 54, 55, 56, 57, 58, 59, 60 and 61	IMVS
10	*E. coli* type strains for O serotypes 62, 63, 64, 65, 66, 68, 69 and 70	IMVS
11	*E. coli* type strains for O serotypes 74, 75, 76, 77, 78, 79, 80 and 81	IMVS
12	*E. coli* type strains for O serotypes 82, 83, 84, 85, 86, 87, 89 and 90	IMVS
13	*E. coli* type strains for O serotypes 91, 92, 95, 96, 97, 98, 99 and 101	IMVS
14	*E. coli* type strains for O serotypes 103, 104, 105, 106, 107, 108 and 110	IMVS
15	*E. coli* type strains for O serotypes 112, 162, 113, 114, 115, 116, 117 and 118	IMVS
16	*E. coli* type strains for O serotypes 123, 165, 166, 167, 168, 169, 170 and 171	See b
17	*E. coli* type strains for O serotypes 172, 173, 127, 128, 129, 130, 131 and 132	See c
18	*E. coli* type strains for O serotypes 133, 134, 135, 136, 140, 141, 142 and 143	IMVS
19	*E. coli* type strains for O serotypes 144, 145, 146, 147, 148, 150, 151 and 152	IMVS

*

a. Institute of Medical and Veterinary Science, Adelaide, Australia

b. 123 from IMVS; the rest from Statens Serum Institut, Copenhagen, Denmark

c. 172 and 173 from Statens Serum Institut, Copenhagen, Denmark, the rest from IMVS

TABLE 5

Pool No.	Strains of which chromosonal DNA included in the pool	Source*
20	*E. coli* type strains for O serotypes 153, 154, 155, 156, 157, 158 , 159 and 160	IMVS
21	*E. coli* type strains for O serotypes 161, 163, 164, 8, 9 and 124	IMVS
22	As pool #21, plus *E. coli* 0111 type strain Stoke W.	IMVS
23	As pool #21, plus *E. coli* 0111:H2 strain C1250-1991	See d
24	As pool #21, plus *E. coli* 0111:H12 strain C156-1989	See e
25	As pool #21, plus *S. enterica* serovar Adelaide	See f
26	*Y. pseudotuberculosis* strains of O groups IA, IIA, IIB, IIC, III, IVA, IVB, VA, VB, VI and VII	See g
27	*S. boydii* strains of serogroups 1, 3, 4, 5, 6, 8, 9, 10, 11, 12, 14 and 15	See h
28	*S. enterica* strains of serovars (each representing a different O group) Typhi, Montevideo, Ferruch, Jangwani, Raus, Hvittingfoss, Waycross, Dan, Dugbe, Basel, 65,:i:e,n,z,15 and 52:d:e,n,x,z15	IMVS

*

d. C1250-1991 from Statens Serum Institut, Copenhagen, Denmark
e. C156-1989 from Statens Serum Institut, Copenhagen, Denmark
f. *S. enterica* serovar Adelaide from IMVS
g. Dr S Aleksic of Institute of Hygiene, Germany
h. Dr J Lefebvre of Bacterial Identification Section, Laboratoroie de Santè Publique du Quèbec, Canada

TABLE 6

Pool No.	Strains of which chromosonal DNA included in the pool	Source*
29	*E. coli* type strains for O serotypes 153, 154, 155, 156, 158, 159 and 160	IMVS
30	*E. coli* type strains for O serotypes 161, 163, 164, 8, 9, 111 and 124	IMVS
31	As pool #29, plus *E. coli* O157 type strain A2 (O157:H19)	IMVS
32	As pool #29, plus *E. coli* O157:H16 strain C475-89	See d
33	As pool #29, plus *E. coli* O157:H45 strain C727-89	See d
34	As pool #29, plus *E. coli* O157:H2 strain C252-94	See d
35	As pool #29, plus *E. coli* O157:H39 strain C258-94	See d
36	As pool #29, plus *E. coli* O157:H26	See e
37	As pool #29, plus *S. enterica* serovar Landau	See f
38	As pool #29, plus *Brucella abortus*	See g See h
39	As pool #29, plus *Y. enterocolitica* O9	
40	*Y. pseudotuberculosis* strains of O groups IA, IIA, IIB, IIC, III, IVA, IVB, VA, VB, VI and VII	See i
41	*S. boydii* strains of serogroups 1, 3, 4, 5, 6, 8, 9, 10, 11, 12, 14 and 15	See j
42	*S. enterica* strains of serovars (each representing a different O group) Typhi, Montevideo, Ferruch, Jangwani, Raus, Hvittingfoss, Waycross, Dan, Dugbe, Basel, 65:i:e,n,z15 and 52:d:e,n,x,z15	IMVS
43	*E. coli* type strains for O serotypes 1,2,3,4,10,18 and 29	IMVS
44	As pool #43, plus *E. coli* K-12 strains C600 and WG1	IVMS See k

*

d. O157 strains from Statens Serum Institut, Copenhagen, Denmark

e. O157:H26 from Dr R Brown of Royal Children's Hospital, Melbourne, Victoria

f. *S. enterica* serovar Landau from Dr M Poppoff of Institut Pasteur, Paris, France

g. *B. Abortus* from the culture collection of The University of Sydney, Sydney, Australia

h. *Y. enterocolitica* O9 from Dr. K. Bettelheim of Victorian Infectious Diseases Reference Laboratory Victoria, Australia.

i. Dr S Aleksic of Institute of Hygiene, Germany

J. Dr J Lefebvre of Bacterial Identification Section, Laboratoroie de Santè Publique du Quèbec, Canada

k. Strains C600 and WG1 from Dr. B.J. Backmann of Department of Biology, Yale University, USA.

TABLE 7 PCR assay result using primers based on the E. coli serotype O16 (strain K-12) O antigen gene cluster sequence

Gene	Function	Base positions of the gene	Forward primer (base positions)	Reverse primer (base positions)	Length of the PCR fragment	Number of pools (out of 21) giving band of correct size	Annealing temperature of the PCR
*rmlB**	TDP-rhamnose pathway	90-1175	#1064(91-109)	#1065(1175-1157)	1085bp	17	60°C
*rmlD**	TDP-rhamnose pathway	1175-2074	#1066(1175-1193)	#1067 (2075-2058)	901bp	13	60°C
*rmlA**	TDP-rhamnose pathway	2132-3013	#1068(2131-2148)	#1069(3013-2995)	883bp	0	60°C
*rmlC**	TDP-rhamnose pathway	3013-3570	#1070(3012-3029)	#1071(3570-3551)	559bp	0	60°C
*gtf**	Galactofuranose pathway	4822-5925	#1074(4822-4840)	#1075(5925-5908)	1104bp	0	55°C
*wzx**	Flippase	3567-4814	#1072(3567-3586)	#1073(4814-4797)	1248bp	0	55°C
*wzy**	O polymerase	5925-7091	#1076(5925-5944)	#1077(7091-7074)	1167bp	0	60°C
*wbbI**	Galactofuranosyl transferase	7094-8086	#1078 (7094-7111)	#1079(8086-8069)	993bp	0	50°C
*wbbJ**	Acetyltransferase	8067-8654	#1080(8067-8084)	#1081(8654-8632)	588bp	0	60°C
*wbbK***	Glucosyl transferase	5770-6888	#1082(5770-5787)	#1083(6888-6871)	1119bp	0	55°C
*wbbL****	Rhamanosyltransferase	679-1437	#1084(679-697)	#1085(1473-1456)	795bp	0****	55°C

*, **, *** Base positions based on GenBank entry U09876, U03041 and L19537 respectively
**** 19 pools giving a band of wrong size

TABLE 8 PCR assay data using 0111 primers

Gene	Base positions of the gene according to SEQ ID NO: 1	Forward primer (base positions)	Reverse primer (base positions)	Length of the PCR fragment	Number of pools (out of 21) giving band of correct size	Annealing temperature of the PCR
wbdH	739-1932	#866 (739-757)	#867(1941-1924)	1203bp	0	60°C
		#976(925-942)	#978(1731-1714)	807bp	0	60°C
		#976(925-942)	#979(1347-1330)	423bp	0	60°C
		#977(1165-1182)	#978(1731-1714)	567bp	0	60°C
wzx	8646-9911	#969(8646-8663)	#970(9908-9891)	1263bp	0	50°C
		#1060(8906-8923)	#1062(9468-9451)	563bp	0	60°C
		#1061(9150-9167)	#1063 (9754-9737)	605bp	0	50°C
wzy	9901-10953	#900(9976-9996)	#901(10827-10807)	852bp	0	60°C
		#980(10113-10130)	#983(10484-10467)	372bp	0*	61°C
wbdL	10931-11824	#870(10931-10949)	#871(11824-11796)	894bp	7	60°C
wbdM	11821-12945	#868(11821-11844)	#869(12945-12924)	1125bp	0	60°C
		#984(12042-12059)	#987(12447-12430)	406bp	0	60°C
		#985(12258-12275)	#986(12698-12681)	441bp	0**	65°C

* Giving a band of wrong size in all pools

** One pool giving a band of wrong size

TABLE 8A PCR specificity test data using 0111 primers

Gene	Base positions of the gene according to SEQ ID NO: 1	Forward primer (base positions)	Reverse primer (base positions)	Length of the PCR fragment	Number of pools (pools no. 25-28) giving band of correct size	Annealing temperature of the PCR
wbdH	739-1932	#866 (739-757)	#867(1941-1924)	1203bp	0*	60°C
		#976(925-942)	#978(1731-1714)	807bp	0	60°C
		#976(925-942)	#979(1347-1330)	423bp	0	60°C
		#977(1165-1182)	#978(1731-1714)	567bp	0	60°C
wzx	8646-9911	#969(8646-8663)	#970(9908-9891)	1263bp	0	55°C
		#1060(8906-8923)	#1062(9468-9451)	563bp	0	60°C
		#1061(9150-9167)	#1063 (9754-9737)	605bp	0*	50°C
wzy	9901-10953	#900(9976-9996)	#901(10827-10807)	852bp	0	60°C
		#980(10113-10130)	#983(10484-10467)	372bp	0**	60°C
wbdL	10931-11824	#870(10931-10949)	#871(11824-11796)	894bp	0	60°C
wbdM	11821-12945	#868(11821-11844)	#869(12945-12924)	1125bp	0	60°C
		#984(12042-12059)	#987(12447-12430)	406bp	0	60°C
		#985(12258-12275)	#986(12698-12681)	441bp	0*	65°C

* 1 pool giving a band of wrong size

** 2 pools giving 3 bands of wrong sizes, 1 pool giving 2 bands of wrong sizes

TABLE 9 PCR results using primers based on the *E. coli* O157 sequence

Gene	Function	Base position of the gene according to SEQ ID NO: 2	Forward primer (base positions)	Reverse primer (base positions)	Length of the PCR fragment	Number of pools (out of 21) giving band of correct size	Annealing temperature of the PCR
wbdN	Sugar transferase	79-861	#1197(79-96)	#1198 (861-844)	783	0	55°C
			#1199(184-201)	#1200(531-514)	348	0	55°C
			#1201(310-327)	#1202(768-751)	459	0	55°C
wzy	O antigen	858-2042	#1203(858-875)	#1204(2042-2025)	1185	0*	50°C
			#1205(1053-1070)	#1206(1619-1602)	567	0	63°C
			#1207(1278-1295)	#1208(1913-1896)	636	0	60°C
wbdO	Sugar transferase	2011-2757	#1209(2011-2028)	#1210(2757-2740)	747	0	50°C
			#1211(2110-2127)	#1212(2493-2476)	384	0**	62°C
			#1213(2305-2322)	#1214(2682-2665)	378	0	60°C
wzx	O antigen flippase	2744-4135	#1215(2744-2761)	#1216(4135-4118)	1392	0	50°C
			#1217(2942-2959)	#1218(3628-3611)	687	O***	63°C
wbdP	Sugar transferase	5257-6471	#1221(5257-5274)	#1222(6471-6454)	1215	0	55°C
			#1223(5440-5457)	#1224(5973-5956)	534	0	55°C
			#1225(5707-5724)	#1226(6231-6214)	525	0	55°C
wbdR	N-acetyl	13156-13821	#1229(13261-13278)	#1230(13629-13612)	369	0	55°C
			#1231(13384-13401)	#1232(13731-13714)	348	0	60°C

* 3 bands of wrong size in one pool, 1 band of wrong size in all other pools

** 3 bands of wrong sizes in 9 pools, 2 bands of wrong size in all other pools

*** 2 bands of wrong sizes in 2 pools, 1 band of wrong size in 7 pools

TABLE 9A PCR results using primers based on the *E. coli* O157 sequence

Gene	Function	Base position of the gene according to SEQ ID NO: 2	Forward primer (base positions)	Reverse primer (base positions)	Length of the PCR fragment	Number of pools (pools no. 37-42) giving band of correct size	Annealing temperature of the PCR
wbdN	Sugar transferase	79-861	#1197(79-96)	#1198 (861-844)	783	0*	55°C
			#1199(184-201)	#1200(531-514)	348	0*	55°C
			#1201(310-327)	#1202(768-751)	459	0	61°C
wzy	O antigen	858-2042	#1203(858-875)	#1204(2042-2025)	1185	1**	50°C
			#1205(1053-1070)	#1206(1619-1602)	567	0***	60°C
			#1207(1278-1295)	#1208(1913-1896)	636	0	60°C
wbdO	Sugar transferase	2011-2757	#1209(2011-2028)	#1210(2757-2740)	747	0	50°C
			#1211(2110-2127)	#1212(2493-2476)	384	0****	61°C
			#1213(2305-2322)	#1214(2682-2665)	378	0	60°C
wzx	O antigen flippase	2744-4135	#1215(2744-2761)	#1216(4135-4118)	1392	0	50°C
			#1217(2942-2959)	#1218(3628-3611)	687	0	63°C
wbdP	Sugar transferase	5257-6471	#1221(5257-5274)	#1222(6471-6454)	1215	0	55°C
			#1223(5440-5457)	#1224(5973-5956)	534	0*	60°C
			#1225(5707-5724)	#1226(6231-6214)	525	0	55°C
wbdR	N-acetyl transferase	13156-13821	#1229(13261-13278)	#1230(13629-13612)	369	0	50°C
			#1231(13384-13401)	#1232(13731-13714)	348	0	60°C

* 1 band of wrong size in one pool
** pool #39 giving two bands, one band of correct size, the other band of wrong size in another pool.
*** 2 bands of wrong sizes in one pool
**** 3 bands of wrong sizes in 2 pools, 2 bands of wrong sizes in 2 other pools

CLAIMS:

1. A nucleic acid molecule encoding all or part of an *E. coli* flagellin protein, provided that the nucleic acid molecule does not encode a protein expressed by the *E. coli* H1, H7, H12 or H48 type strains.

2. A nucleic acid molecule according to claim 1 wherein the molecule is derived from a *fliC* gene.

3. A nucleic acid molecule including all or part of a sequence according to any one of SEQ ID NOs:1 to 68.

4. A nucleic acid molecule consisting of all or part of a sequence according to any one of SEQ ID NOs: 1 to 68.

5. A nucleic acid molecule according to any one of claims 1-4 wherein the molecule is from about 10 to 20 nucleotides in length.

6. A nucleic acid molecule according to claim 5 wherein the molecule is capable of hybridising to the central region of a flagellin gene from which the molecule is derived.

7. A nucleic acid molecule selected from the group of nucleic acid molecules shown in Table 3.

8. A method of detecting the presence of *E. coli* of a particular H serotype in a sample, the method comprising the step of specifically hybridising at least one nucleic acid molecule derived from a flagellin gene, wherein the at least one nucleic acid molecule is specific for a particular flagellin gene associated with the H serotype, to any *E. coli* in the sample which contain the gene, and detecting any specifically hybridised nucleic acid molecules, wherein the presence of specifically

hybridised nucleic acid molecules identifies the presence of the H serotype in the sample.

9. A method according to claim 8 wherein the at least one nucleic acid molecule is according to any one of claims 1 to 7.

10. A method according to claim 8 wherein the specifically hybridised nucleic acid molecules are detected by Southern Blot analysis.

11. A method of detecting the presence of *E. coli* of a particular H serotype in a sample, the method comprising the step of specifically hybridising at least one pair of nucleic acid molecules to any *E. coli* in the sample which contains the flagellin gene for the particular H serotype, wherein at least one of the nucleic acid molecules is specific for the particular flagellin gene associated with the H serotype, and detecting any specifically hybridised nucleic acid molecules, wherein the presence of specifically hybridised nucleic acid molecules identifies the presence of the H serotype in the sample.

12. A method according to claim 11 wherein the at least one pair of nucleic acid molecules is according to any one of claims 1 to 7.

13. A method according to claim 11 wherein the specifically hybridised nucleic acid molecules are detected by the polymerase chain reaction.

14. A method for detecting the presence of a particular O serotype and H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) specifically hybridising at least one nucleic acid molecule derived from and specific for a gene

encoding a transferase or a gene encoding an enzyme for the transport or processing of a polysaccharide or oligosaccharide unit, the gene being involved in the synthesis of a particular *E. coli* O antigen, to any *E. coli* in the sample which contain the gene;

(b) specifically hybridising at least one nucleic acid molecule derived from and specific for a particular flagellin gene associated with that H serotype, to any *E. coli* in the sample which contain the gene; and

(c) detecting any specifically hybridised nucleic acid molecules, wherein the presence of specifically hybridised nucleic acid molecules identifies the presence of the particular H serotype and O serotype of *E. coli* in the sample.

15. A method according to claim 14 wherein the at least one nucleic acid molecule of step (a) is selected from the group consisting of:
wbdH (nucleotide position 739 to 1932 of Figure 5),
wzx (nucleotide position 8646 to 9911 of Figure 5),
wzy (nucleotide position 9901 to 10953 of Figure 5),
wbdM (nucleotide position 11821 to 12945 of Figure 5),
wbdN (nucleotide position 79 to 861 of Figure 6),
wbdO (nucleotide position 2011 to 2757 of Figure 6),
wbdP (nucleotide position 5257 to 6471 of Figure 6),
wbdR (nucleotide position 13156 to 13821 of Figure 6),
wzx (nucleotide position 2744 to 4135 of Figure 6) and
wzy (nucleotide position 858 to 2042 of Figure 6).

16. A method according to claim 14 wherein the at least one nucleic acid molecule of step (a) is selected from the group of nucleic acid molecules shown in Tables 8, 8A, 9 and 9A.

17. A method according to claim 14 wherein the at least one nucleic acid molecule of step (b) is according to any one of claims 1 to 7.

18. A method according to claim 14 wherein the specifically hybridised nucleic acid molecules are detected by Southern Blot analysis.

19. A method for detecting the presence of a particular O serotype and H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) specifically hybridising at least one pair of nucleic acid molecules derived from and specific for a gene encoding a transferase or a gene encoding an enzyme for the transport or processing of a polysaccharide or oligosaccharide unit, the gene being involved in the synthesis of a particular *E. coli* O antigen, to any *E. coli* in the sample which contain the gene;

(b) specifically hybridising at least one pair of nucleic acid molecules derived from and specific for a particular flagellin gene associated with that H serotype, to any *E. coli* in the sample which contain the gene; and

(c) detecting any specifically hybridised nucleic acid molecules, wherein the presence of specifically hybridised nucleic acid molecules identifies the presence of the particular H serotype and O serotype of *E. coli* in the sample.

20. A method according to claim 19 wherein the at least one pair of nucleic acid molecules of step (a) is selected from the group consisting of:
wbdH (nucleotide position 739 to 1932 of Figure 5),
wzx (nucleotide position 8646 to 9911 of Figure 5),
wzy (nucleotide position 9901 to 10953 of Figure 5),
wbdM (nucleotide position 11821 to 12945 of Figure 5),
wbdN (nucleotide position 79 to 861 of Figure 6),
wbdO (nucleotide position 2011 to 2757 of Figure 6),
wbdP (nucleotide position 5257 to 6471 of Figure 6),
wbdR (nucleotide position 13156 to 13821 of Figure 6),

wzx (nucleotide position 2744 to 4135 of Figure 6) and *wzy* (nucleotide position 858 to 2042 of Figure 6).

21. A method according to claim 19 wherein the at least one pair of nucleic acid molecules of step (a) is selected from the group of nucleic acid molecules shown in Tables 8, 8A, 9 and 9A.

22. A method according to claim 19 wherein the at least one nucleic acid molecule of step (b) is according to any one of claims 1 to 7.

23. A method according to claim 19 wherein the specifically hybridised nucleic acid molecules are detected by the polymerase chain reaction.

24. A method for detecting the presence of a particular O serotype and H serotype of *E. coli* in a sample, the method comprising the following steps:

(a) specifically hybridising at least one nucleic acid molecule derived from and specific for a gene encoding a flagellin associated with a particular *E. coli* H antigen serotype, to any *E. coli* carrying the gene and present in the sample;

and

(b) detecting the at least one specifically hybridised nucleic acid molecule, wherein the at least one nucleic acid molecule is specific for the particular combination of O and H antigen.

25. A method according to claim 24 wherein the at least nucleic acid molecule is according to any one of SEQ ID NOS: 9, 55, 57 to 65.

26. A method for testing a food derived sample for the presence of one or more particular *E. coli* O antigens and H antigens, wherein the particular *E. coli* O and H

antigens in the food derived sample are detected using the method of any one of claims 8, 11, 14 or 19.

27. A method for testing a faecal derived sample for the presence of one or more particular *E. coli* O antigens and H antigens wherein the particular *E. coli* O and H antigens in the faecal derived sample are detected using the method of any one of claims 8, 11, 14 or 19.

28. A method for testing a patient or animal derived sample for the presence of one or more particular *E. coli* O antigens and H antigens wherein the particular *E. coli* O and H antigens in the patient or animal derived sample are detected using the method of any one of claims 8, 11, 14 or 19.

29. A kit for identifying the H serotype of *E. coli*, the kit comprising at least one nucleic acid molecule according to any one of claims 1 to 7.

30. A kit for identifying the H and O serotype of *E. coli*, the kit comprising:
(a) at least one nucleic acid molecule derived from and specific for an *E. coli* flagellin gene; and
(b) at least one nucleic acid molecule derived from and specific for a gene encoding a transferase or a gene encoding an enzyme for the transport or processing of a polysaccharide or oligosaccharide unit, the gene being involved in the synthesis of a particular *E. coli* O antigen.

31. A kit according to claim 30 wherein the at least one nucleic acid molecule of (a) is selected from the group consisting of:
wbdH (nucleotide position 739 to 1932 of Figure 5), *wzx* (nucleotide position 8646 to 9911 of Figure 5), *wzy* (nucleotide position 9901 to 10953 of Figure 5),

wbdM (nucleotide position 11821 to 12945 of Figure 5), *wbdN* (nucleotide position 79 to 861 of Figure 6), *wbdO* (nucleotide position 2011 to 2757 of Figure 6), *wbdP* (nucleotide position 5257 to 6471 of Figure 6), *wbdR* (nucleotide position 13156 to 13821 of Figure 6), *wzx* (nucleotide position 2744 to 4135 of Figure 6) and *wzy* (nucleotide position 858 to 2042 of Figure 6).

32. A kit according to claim 30 wherein the at least one nucleic acid molecule of (a) is selected from the group of nucleic acid molecules shown in Tables 8, 8A, 9 and 9A.

33. A kit according to claim 30 wherein the at least one nucleic acid molecule of (b) is according to any one of claims 1 to 7.

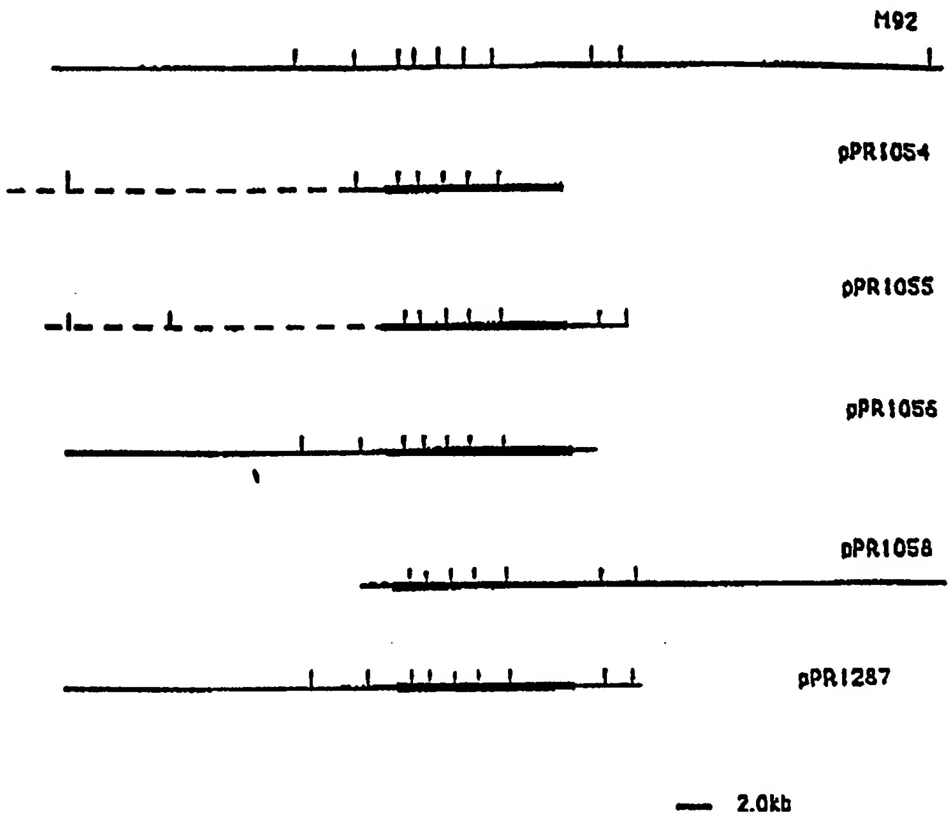

Figure 1

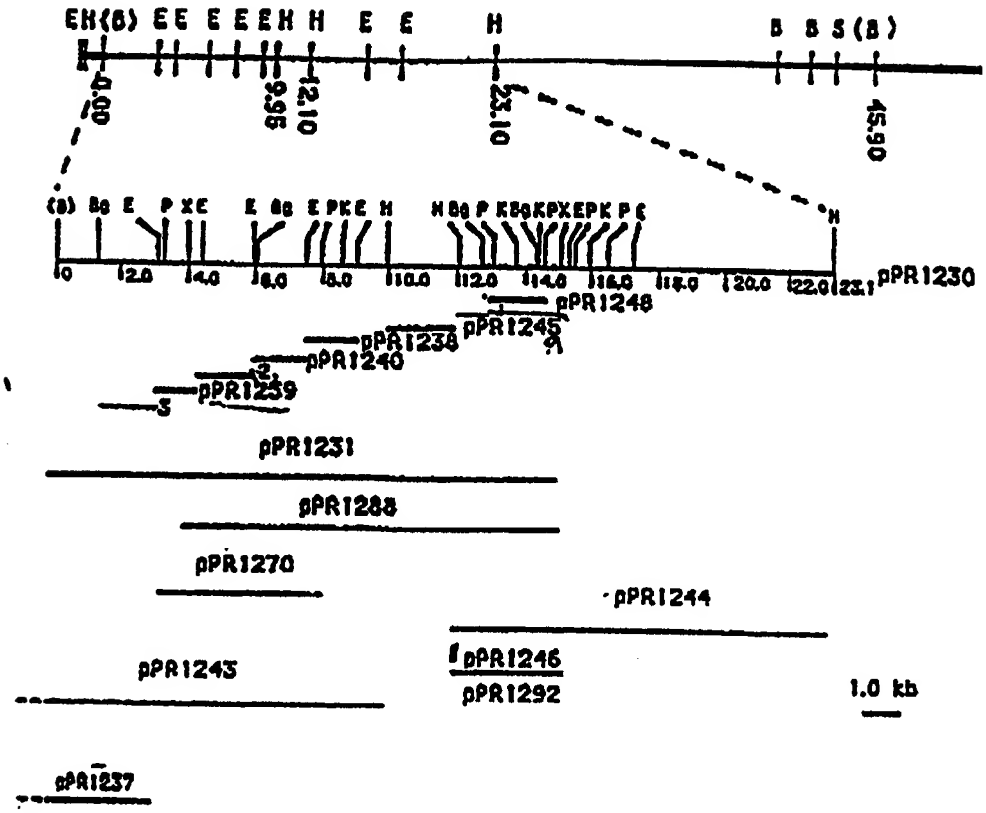
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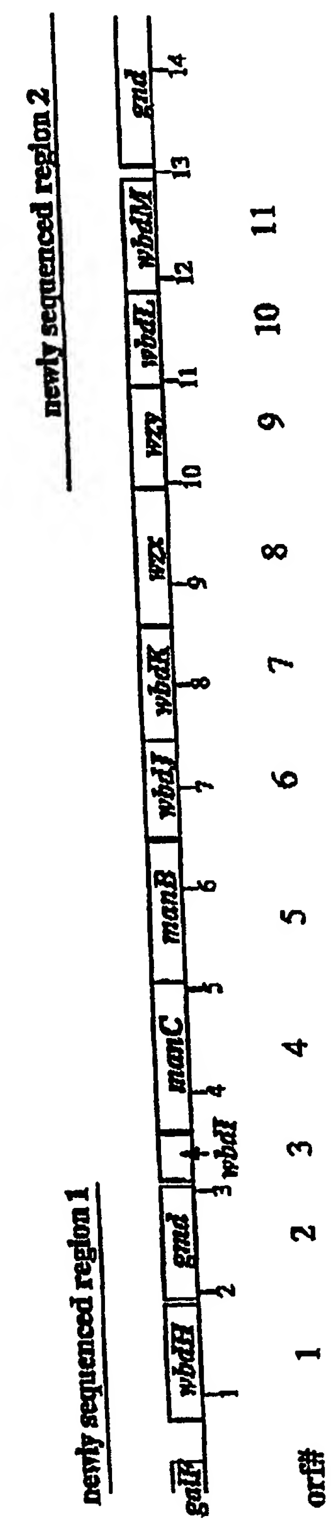
Figure 2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newly sequenced region 2
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manB
wbdJ
wbdK
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6
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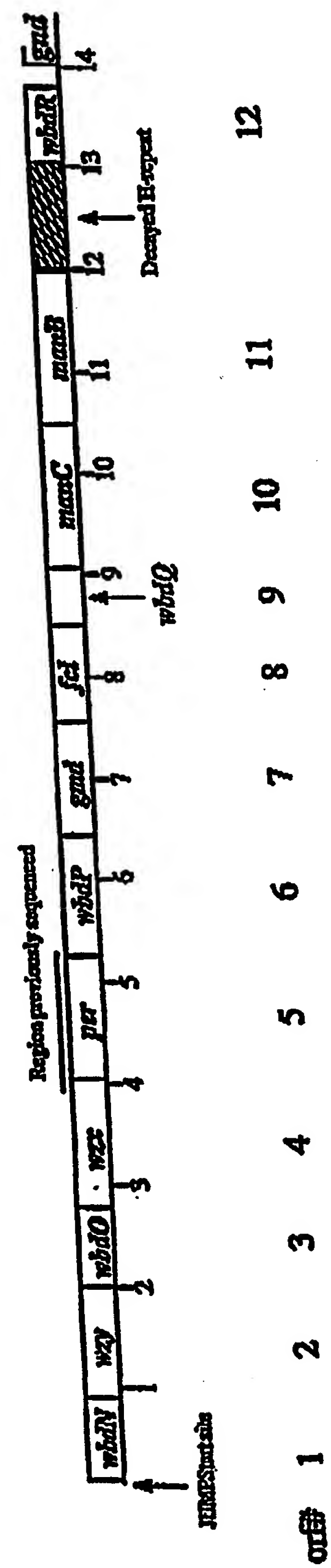
Figure 3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manB
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Region previously sequenced
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wzx
wbdO
wzy
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orf#
1
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4
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6
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8
9
10
11
12

Figure 4

GATCTGATGGCCGTAGGGCGCTACGTGCTTTCTGCTGATATCTGGGCTGAGTTGGAAAAA 60

ACTGCTCCAGGTGCCTGGGGACGTATTCAACTGACTGATGCTATTGCAGAGTTGGCTAAA 120

AAACAGTCTGTTGATGCCATGCTGATGACCGGCGACAGCTACGACTGCGGTAAGAAGATG 180

GGCTATATGCAGGCATTCGTTAAGTATGGGCTGCGCAACCTTAAAGAAGGGGCGAAGTTC 240

CGTAAGAGCATCAAGAAGCTACTGAGTGAGTAGAGATTTACACGTCTTTGTGACGATAAG 300

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TGCCGTTTTTTATGAAAAATGACCAATAATAACAAGTTAACCTACCAAGTTTAATCTGCT 420

TTTTGTTGGATTTTTTCTTGTTTCTGGTCGCATTTGGTAAGACAATTAGCGTGAGTTTTA 480

GAGAGTTTTGCGGGATCTCGCGGAACTGCTCACATCTTTGGCATTTAGTTAGTGCACTGG 540

TAGCTGTTAAGCCAGGGGCGGTAGCTTGCCTAATTAATTTTTAACGTATACATTTATTCT 600

TGCCGCTTATAGCAAATAAAGTCAATCGGATTAAACTTCTTTTCCATTAGGTAAAAGAGT 660

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Start of orf1

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 F  R  K  E  L  I  M  N  L  V  R  Q  G  D  N  V  Y  C  L  A
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 N  D  F  S  T  E  D  L  K  V  L  S  S  W  G  V  K  G  V  K
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 K  K  I  L  K  D  I  S  P  D  I  V  F  S  Y  F  V  K  P  V
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AAGTGGATACAAATTCTTTTATATAAGTTAGCATTACCGATGCTTGATGATTTGATTCTA  1260

 L  N  H  D  D  K  K  D  L  I  D  Q  Y  N  I  K  A  K  V  T
TTAAATCATGATGATAAAAAAGATTTAATCGATCAGTATAATATTAAAGCTAAGGTAACA  1320

 V  L  G  G  I  G  L  D  L  N  E  F  S  Y  K  E  P  P  K  E
GTGTTAGGTGGGATTGGATTGGATCTTAATGAGTTTTCATATAAAGAGCCACCGAAAGAG  1380

 K  I  T  F  I  F  I  A  R  L  L  R  E  K  G  I  F  E  F  I
AAAATTACCTTTATTTTTATAGCAAGGTTATTAAGAGAGAAAGGGATATTTGAGTTTATT  1440

 E  A  A  K  F  V  K  T  T  Y  P  S  S  E  F  V  I  L  G  G
GAAGCCGCAAAGTTCGTTAAGACAACTTATCCAAGTTCTGAATTTGTAATTTTAGGAGGT  1500
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 F  E  S  N  N  P  F  S  L  Q  K  N  E  I  E  S  L  R  K  E
TTTGAGAGTAATAATCCTTTCTCATTACAAAAAAATGAAATTGAATCGCTAAGAAAAGAA    1560

 H  D  L  I  Y  P  G  H  V  E  N  V  Q  D  W  L  E  K  S  S
CATGATCTTATTTATCCTGGTCATGTGGAAAATGTTCAAGATTGGTTAGAGAAAAGTTCT    1620

 V  F  V  L  P  T  S  Y  R  E  G  V  P  R  V  I  Q  E  A  M
GTTTTTGTTTTACCTACATCATATCGAGAAGGCGTACCAAGGGTGATCCAAGAAGCTATG    1680

 A  I  G  R  P  V  I  T  T  N  V  P  G  C  R  D  I  I  N  D
GCTATTGGTAGACCTGTAATAACAACTAATGTACCTGGGTGTAGGGATATAATAAATGAT    1740

 G  V  N  G  F  L  I  P  P  F  E  I  N  L  L  A  E  K  M  K
GGGGTCAATGGCTTTTTGATACCTCCATTTGAAATTAATTTACTGGCAGAAAAAATGAAA    1800

 Y  F  I  E  N  K  D  K  V  L  E  M  G  L  A  G  R  K  F  A
TATTTTATTGAGAATAAAGATAAAGTACTCGAAATGGGGCTTGCTGGAAGGAAGTTTGCA    1860

 E  K  N  F  D  A  F  E  K  N  N  R  L  A  S  I  I  K  S  N
GAAAAAAACTTTGATGCTTTTGAAAAAAATAATAGACTAGCATCAATAATAAAATCAAAT    1920


          End of orf1
 N  D  F  *

AATGATTTTTGACTTGAGCAGAAATTATTTATATTTCAATCTGAAAAAATAAAGGCTGTTA   1980

   Start of orf2
   M  N  K  V  A  L  I  T  G  I  T  G  Q  D  G  S  Y  L  A
TTATGAATAAAGTGGCATTAATTACTGGTATCACTGGGCAAGATGGCTCCTATTTGGCAG    2040

E  L  L  L  E  K  G  Y  E  V  H  G  I  K  R  R  A  S  S  F
AATTATTGTTAGAAAAAGGTTATGAAGTTCATGGTATTAAACGCCGTGCATCTTCATTTA    2100

N  T  E  R  V  D  H  I  Y  Q  D  S  H  L  A  N  P  K  L  F
ATACTGAGCGAGTGGATCACATCTATCAGGATTCACATTTAGCTAATCCTAAACTTTTTC    2160

L  H  Y  G  D  L  T  D  T  S  N  L  T  R  I  L  K  E  V  Q
TACACTATGGCGATTTGACAGATACTTCCAATCTGACCCGTATTTTAAAAGAAGTTCAAC    2220

P  D  E  V  Y  N  L  G  A  M  S  H  V  A  V  S  F  E  S  P
CAGATGAAGTTTACAATTTGGGGGCGATGAGCCATGTAGCGGTATCATTTGAGTCACCAG    2280

E  Y  T  A  D  V  D  A  I  G  T  L  R  L  L  E  A  I  R  I
AATACACTGCTGATGTTGATGCGATAGGAACATTGCGTCTTCTTGAAGCTATCAGGATAT    2340

L  G  L  E  K  K  T  K  F  Y  Q  A  S  T  S  E  L  Y  G  L
TGGGGCTGGAAAAAAAGACAAAATTTTATCAGGCTTCAACTTCAGAGCTTTATGGTTTGG    2400

V  Q  E  I  P  Q  K  E  T  T  P  F  Y  P  R  S  P  Y  A  V
TTCAAGAAATTCCACAAAAAGAGACTACGCCATTTTATCCACGTTCGCCTTATGCTGTTG    2460

A  K  L  Y  A  Y  W  I  T  V  N  Y  R  E  S  Y  G  M  F  A
CAAAATTATATGCCTATTGGATCACTGTTAATTATCGTGAGTCTTATGGTATGTTTGCCT    2520

C  N  G  I  L  F  N  H  E  S  P  R  R  G  E  T  F  V  T  R
GCAATGGTATTCTCTTTAACCACGAATCACCTCGCCGTGGCGAGACCTTTGTTACTCGTA    2580

K  I  T  R  G  I  A  N  I  A  Q  G  L  D  K  C  L  Y  L  G
AAATAACACGCGGGATAGCAAATATTGCTCAAGGTCTTGATAAATGCTTATACTTGGGAA    2640

N  M  D  S  L  R  D  W  G  H  A  K  D  Y  V  K  M  Q  W  M
ATATGGATTCTCTGCGTGATTGGGGACATGCTAAGGATTATGTCAAAATGCAATGGATGA    2700
```

Figure 5

M L Q Q E T P E D F V I A T G I Q Y S V

TGCTGCAGCAAGAAACTCCAGAAGATTTTGTAATTGCTACAGGAATTCAATATTCTGTCC 2760

R E F V T M A A E Q V G I E L A F E G E

GTGAGTTTGTCACAATGGCGGCAGAGCAAGTAGGCATAGAGTTAGCATTTGAAGGTGAGG 2820

G V N E K G V V V S V N G T D A K A V N

GAGTAAATGAAAAAGGTGTTGTTGTTTCGGTCAATGGCACTGATGCTAAAGCTGTAAACC 2880

P G D V I I S V D P R Y F R P A E V E T

CGGGCGATGTAATTATATCTGTAGATCCAAGGTATTTTAGGCCTGCAGAAGTTGAAACCT 2940

L L G D P T N A H K K L G W S P E I T L

TGCTTGGCGATCCTACTAATGCGCATAAAAAATTAGGATGGAGCCCTGAAATTACATTGC 3000

R E M V K E M V S S D L A I A K K N V L

GTGAAATGGTAAAAGAAATG~~GTTTCCAGCGATTTAGCAATAGCGAAAAAGAACGTCTTGC~~ 3060

End of orf2

L K A N N I A T N I P Q E *

~~TGAAAGCTAATAACATTGCCACTAATATTCCGCAAGAATAAAAAAGATAATACATTAAAT~~ 3120

Start of orf3

M F

~~AATTAAAAATGGTGCTAGATTTATTAGTACCATTATTTTTTTTTGGGTGACTAATGTTTA~~ 3180

I T S D K F R E I I K L V P L V S I D L

~~TTACATCAGATAAATTTAGAGAAATTATCAAGTTAGTTCCATTAGTATCAATTGATCTGC~~ 3240

L I E N E N G E Y L F G L R N N R P A K

~~TAATTGAAAACGAGAATGGTGAATATTTATTTGGTCTTAGGAATAATCGACCGGCCAAAA~~ 3300

N Y F F V P G G R I R K N E S I K N A F

~~ATTATTTTTTTGTTCCAGGTGGTAGGATTCGCAAAAATGAATCTATTAAAAATGCTTTTA~~ 3360

K R I S S M E L G K E Y G I S G S V F N

~~AAAGAATATCATCTATGGAATTAGGTAAAGAGTATGGTATTTCAGGAAGTGTTTTTAATG~~ 3420

G V W E H F Y D D G F F S E G E A T H Y

~~GTGTATGGGAACATTTCTATGATGATGGTTTTTTTTCTGAAGGCGAGGCAACACATTATA~~ 3480

I V L C Y T L K V L K S E L N L P D D Q

~~TAGTGCTTTGTTACACACTGAAAGTTCTTAAAAGTGAATTGAATCTCCCAGATGATCAAC~~ 3540

H R E Y L W L T K H Q I N A K Q D V H N

~~ATCGTGAATACCTTTGGCTAACTAAACACCAAATAAATGCTAAACAAGATGTTCATAACT~~ 3600

End of orf3 **Start of orf4**

Y S K N Y F L * M

~~ATTCAAAAAATTATTTTTTGTAATTTTTATTAAAAATTAATATGCGAGAGAATTGTATGT~~ 3660

S Q C L Y P V I I A G G T G S R L W P L

~~CTCAATGTCTTTACCCTGTAATTATTGCCGGAGGAACCGGAAGCCGTCTATGGCCGTTGT~~ 3720

S R V L Y P K Q F L N L V G D S T M L Q

~~CTCGAGTATTATACCCTAAACAATTTTTAAATTTAGTTGGGGATTCTACAATGTTGCAAA~~ 3780

T T I T R L D G I E C E N P I V I C N E

~~CAACAATTACGCGTTTGGATGGCATCGAATGCGAAAATCCAATTGTTATCTGCAATGAAG~~ 3840

D H R F I V A E Q L R Q I G K L T K N I

~~ATCACCGATTTATTGTAGCAGAGCAATTACGACAGATTGGTAAGCTAACCAAGAATATTA~~ 3900

I L E P K G R N T A P A I A L A A F I A

~~TACTTGAGCCGAAAGGCCGTAATACTGCACCTGCCATAGCTTTAGCTGCTTTTATCGCTC~~ 3960

Figure 5

Q K N N P N D D P L L L V L A A D H S I
AGAAGAATAATCCTAATGACGACCCTTTATTATTAGTACTTGCGGCAGACCACTCTATAA 4020

N N E K A F R E S I I K A M P Y A T S G
ATAATGAAAAAGCATTTCGAGAGTCAATAATAAAAGCTATGCCGTATGCAACTTCTGGGA 4080

K L V T F G I I P D T A N T G Y G Y I K
AGTTAGTAACATTTGGAATTATTCCGGACACGGCAAATACTGGTTATGGATATATTAAGA 4140

R S S S A D P N K E F P A Y N V A E F V
GAAGTTCTTCAGCTGATCCTAATAAAGAATTCCCAGCATATAATGTTGCGGAGTTTGTAG 4200

E K P D V K T A Q E Y I S S G N Y Y W N
AAAAACCAGATGTTAAAACAGCACAGGAATATATTTCGAGTGGGAATTATTACTGGAATA 4260

S G M F L F R A S K Y L D E L R K F R P
GCGGAATGTTTTTATTTCGCGCCAGTAAATATCTTGATGAACTACGGAAATTTAGACCAG 4320

D I Y H S C E C A T A T A N I D M D F V
ATATTTATCATAGCTGTGAATGTGCAACCGCTACAGCAAATATAGATATGGACTTTGTCC 4380

R I N E A E F I N C P E E S I D Y A V M
GAATTAACGAGGCTGAGTTTATTAATTGTCCTGAAGAGTCTATCGATTATGCTGTGATGG 4440

E K T K D A V V L P I D I G W N D V G S
AAAAAACAAAAGACGCTGTAGTTCTTCCGATAGATATTGGCTGGAATGACGTGGGTTCTT 4500

W S S L W D I S Q K D C H G N V C H G D
GGTCATCACTTTGGGATATAAGCCAAAAGGATTGCCATGGTAATGTGTGCCATGGGGATG 4560

V L N H D G E N S F I Y S E S S L V A T
TGCTCAATCATGATGGAGAAAATAGTTTTATTTACTCTGAGTCAAGTCTGGTTGCGACAG 4620

V G V S N L V I V Q T K D A V L V A D R
TCGGAGTAAGTAATTTAGTAATTGTCCAAACCAAGGATGCTGTACTGGTTGCGGACCGTG 4680

D K V Q N V K N I V D D L K K R K R A E
ATAAAGTCCAAAATGTTAAAAACATAGTTGACGATCTAAAAAAGAGAAAACGTGCTGAAT 4740

Y Y M H R A V F R P W G K F D A I D Q G
ACTACATGCATCGTGCAGTTTTTCGCCCTTGGGGTAAATTCGATGCAATAGACCAAGGCG 4800

D R Y R V K K I I V K P G E G L D L R M
ATAGATATAGAGTAAAAAAAATAATAGTTAAACCAGGAGAAGGGTTAGATTTAAGGATGC 4860

H H H R A E H W I V V S G T A K V S L G
ATCATCATAGGGCAGAGCATTGGATTGTTGTATCCGGTACTGCTAAAGTTTCACTAGGTA 4920

S E V K L L V S N E S I Y I P Q G A K Y
GTGAAGTTAAACTATTAGTTTCTAATGAGTCTATATATATCCCTCAGGGAGCAAAATATA 4980

S L E N P G V I P L H L I E V S S G D Y
GTCTTGAGAATCCAGGCGTAATACCTTTGCATCTAATTGAAGTAAGTTCTGGTGATTACC 5040

L E S D D I V R F T D R Y N S K Q F L K
TTGAATCAGATGATATAGTGCGTTTTACTGACAGATATAACAGTAAACAATTCCTAAAGC 5100

End of orf4 Start of orf5

M N K I T C F K A Y D I R G R L
R D *
GAGATTGATAAATATGAATAAAATAACTTGCTTCAAAGCATATGATATACGTGGGCGTCT 5160

Figure 5(d)

G A E L N D E I A Y R I G R A Y G E F F
~~TGGTGCTGAATTGAATGATGAAATAGCATATAGAATTGGTCGCGCTTATGGTGAGTTTTT~~ 5220

K P Q T V V V G G D A R L T S E S L K K
~~TAAACCTCAAACTGTAGTTGTGGGAGGAGATGCTCGCTTAACAAGTGAGAGTTTAAAGAA~~ 5280

S L S N G L C D A G V N V L D L G M C G
~~ATCACTCTCAAATGGGCTATGTGATGCAGGCGTAAATGTCTTAGATCTTGGAATGTGTGG~~ 5340

T E E I Y F S T W Y L G I D G G I E V T
~~TACTGAAGAGATATATTTTTCCACTTGGTATTTAGGAATTGATGGTGGAATCGAGGTAAC~~ 5400

A S H N P I D Y N G M K L V T K G A R P
~~TGCAAGCCATAATCCAATTGATTATAATGGAATGAAATTAGTAACCAAAGGTGCTCGACC~~ 5460

I S S D T G L K D I Q Q L V E S N N F E
~~AATCAGCAGTGACACAGGTCTCAAAGATATACAACAATTAGTAGAGAGTAATAATTTTGA~~ 5520

E L N L E K K G N I T K Y S T R D A Y I
~~AGAGCTCAACCTAGAAAAAAAAGGGAATATTACCAAATATTCCACCCGAGATGCCTACAT~~ 5580

N H L M G Y A N L Q K I K K I K I V V N
~~AAATCATTTGATGGGCTATGCTAATCTGCAAAAAATAAAAAAAATCAAAATAGTTGTGAA~~ 5640

S G N G A A G P V I D A I E E C F L R N
~~TTCTGGGAATGGTGCAGCTGGTCCTGTTATTGATGCTATTGAGGAATGCTTTTTACGGAA~~ 5700

N I P I Q F V K I N N T P D G N F P H G
~~CAATATTCCGATTCAGTTTGTAAAAATAAATAATACACCCGATGGTAATTTTCCACATGG~~ 5760

I P N P L L P E C R E D T S S A V I R H
~~TATCCCTAATCCATTACTACCTGAGTGCAGAGAAGATACCAGCAGTGCGGTTATAAGACA~~ 5820

S A D F G I A F D G D F D R C F F F D E
~~TAGTGCTGATTTTGGTATTGCATTTGATGGTGATTTTGATAGGTGTTTTTTCTTTGATGA~~ 5880

N G Q F I E G Y Y I V G L L A E V F L G
~~AAATGGACAATTTATTGAAGGATACTACATTGTTGGTTTATTAGCGGAAGTTTTTTTAGG~~ 5940

K Y P N A K I I H D P R L I W N T I D I
~~GAAATATCCAAACGCAAAAATCATTCATGATCCTCGCCTTATATGGAATACTATTGATAT~~ 6000

V E S H G G I P I M T K T G H A Y I K Q
~~CGTAGAAAGTCATGGTGGTATACCTATAATGACTAAAACCGGTCATGCTTACATTAAGCA~~ 6060

R M R E E D A V Y G G E M S A H H Y F K
~~AAGAATGCGTGAAGAGGATGCCGTATATGGCGGCGAAATGAGTGCGCATCATTATTTTAA~~ 6120

D F A Y C D S G M I P W I L I C E L L S
~~AGATTTTGCATACTGCGATAGTGGAATGATTCCTTGGATTTTAATTTGTGAACTTTTGAG~~ 6180

L T N K K L G E L V C G C I N D W P A S
~~TCTGACAAATAAAAAATTAGGTGAACTGGTTTGTGGTTGTATAAACGACTGGCCGGCAAG~~ 6240

G E I N C T L D N P Q N E I D K L F N R
~~TGGAGAAATAAACTGTACACTAGACAATCCGCAAAATGAAATAGATAAATTATTTAATCG~~ 6300

Y K D S A L A V D Y T D G L T M E F S D
~~TTACAAAGATAGTGCCTTAGCTGTTGATTACACTGATGGATTAACTATGGAGTTCTCTGA~~ 6360

W R F N V R C S N T E P V V R L N V E S
~~TTGGCGTTTTAATGTTAGATGCTCAAATACAGAACCTGTAGTACGATTGAATGTAGAATC~~ 6420

R N N A I L M Q E K T E E I L N F I S K
~~TAGGAATAATGCTATTCTTATGCAGGAAAAAACAGAAGAAATTCTGAATTTTATATCAAA~~ 6480

Figure 5(c)

End of orf5 **Start of orf6**

* M K V L L T G

~~ATAAATTTGCACCTGAGTTCATAATGGAACAAGAAATATATGAAAGTACTTCTGACTGG~~ 6540

S T G M V G K N I L E H D S A S K Y N I

~~CTCAACTGGCATGGTTGGTAAGAATATATTAGAGCATGATAGTGCAAGTAAATATAATAT~~ 6600

L T P T S S D L N L L D K N E I E K F M

~~ACTTACTCCAACCAGCTCTGATTTGAATTTATTAGATAAAAATGAAATAGAAAAATTCAT~~ 6660

L I N M P D C I I H A A G L V G G I H A

~~GCTTATCAACATGCCAGACTGTATTATACATGCAGCGGGATTAGTTGGAGGCATTCATGC~~ 6720

N I S R P F D F L E K N L Q M G L N L V

~~AAATATAAGCAGGCCGTTTGATTTTCTGGAAAAAAATTTGCAGATGGGTTTAAATTTAGT~~ 6780

S V A K K L G I K K V L N L G S S C M Y

~~TTCCGTCGCAAAAAAACTAGGTATCAAGAAAGTGCTTAACTTGGGTAGTTCATGCATGTA~~ 6840

P K N F E E A I P E K A L L T G E L E E

~~CCCCAAAAACTTTGAAGAGGCTATTCCTGAGAAAGCTCTGTTAACTGGTGAGCTAGAAGA~~ 6900

T N E G Y A I A K I A V A K A C E Y I S

~~AACTAATGAGGGATATGCTATTGCGAAAATTGCTGTAGCAAAAGCATGCGAATATATATC~~ 6960

R E N S N Y F Y K T I I P C N L Y G K Y

~~AAGAGAAAACTCTAATTATTTTTATAAAACAATTATCCCATGTAATTTATATGGGAAATA~~ 7020

D K F D D N S S H M I P A V I K K I H H

~~TGATAAATTTGATGATAACTCGTCACATATGATTCCGGCAGTTATAAAAAAAATCCATCA~~ 7080

A K I N N V P E I E I W G D G N S R R E

~~TGCGAAAATTAATAATGTCCCAGAGATCGAAATTTGGGGGGATGGTAATTCGCGCCGTGA~~ 7140

F M Y A E D L A D L I F Y V I P K I E F

~~GTTTATGTATGCAGAAGATTTAGCTGATCTTATTTTTTATGTTATTCCTAAAATAGAATT~~ 7200

M P N M V N A G L G Y D Y S I N D Y Y K

~~CATGCCTAATATGGTAAATGCTGGTTTAGGTTACGATTATTCAATTAATGACTATTATAA~~ 7260

I I A E E I G Y T G S F S H D L T K P T

~~GATAATTGCAGAAGAAATTGGTTATACTGGGAGTTTTTCTCATGATTTAACAAAACCAAC~~ 7320

G M K R K L V D I S L L N K I G W S S H

~~AGGAATGAAACGGAAGCTAGTAGATATTTCATTGCTTAATAAAATTGGTTGGTCAAGTCA~~ 7380

F E L R D G I R K T Y N Y Y L E N Q N K

~~CTTTGAACTCAGAGATGGCATCAGAAAGACCTATAATTATTACTTGGAGAATCAAAATAA~~ 7440

Start of orf7, End of orf6

M I T Y P L A S N T W D E Y E Y A A I Q

*

~~ATGATTACATACCCACTTGCTAGTAATACTTGGGATGAATATGAGTATGCAGCAATACAG~~ 7500

S V I D S K M F T M G K K V E L Y E K N

~~TCAGTAATTGACTCAAAAATGTTTACCATGGGTAAAAAGGTTGAGTTATATGAGAAAAAT~~ 7560

F A D L F G S K Y A V M V S S G S T A N

~~TTTGCTGATTTGTTTGGTAGCAAATATGCCGTAATGGTTAGCTCTGGTTCTACAGCTAAT~~ 7620

Figure 5 (f)

L L M I A A L F F T N K P K L K R G D E
~~CTGTTAATGATTGCTGCCCTTTTCTTCACTAATAAACCAAAACTTAAAAGAGGTGATGAA~~ 7680

I I V P A V S W S T T Y Y P L Q Q Y G L
~~ATAATAGTACCTGCAGTGTCATGGTCTACGACATATTACCCTCTGCAACAGTATGGCTTA~~ 7740

K V K F V D I N K E T L N I D I D S L K
~~AAGGTGAAGTTTGTCGATATCAATAAAGAAACTTTAAATATTGATATCGATAGTTTGAAA~~ 7800

N A I S D K T K A I L T V N L L G N P N
~~AATGCTATTTCAGATAAAACAAAAGCAATATTGACAGTAAATTTATTAGGTAATCCTAAT~~ 7860

D F A K I N E I I N N R D I I L L E D N
~~GATTTTGCAAAAATAAATGAGATAATAAATAATAGGGATATTATCTTACTAGAAGATAAC~~ 7920

C E S M G A V F Q N K Q A G T F G V M G
~~TGTGAGTCGATGGGCGCGGTCTTTCAAAATAAGCAGGCAGGCACATTCGGAGTTATGGGT~~ 7980

T F S S F Y S H H I A T M E G G C V V T
~~ACCTTTAGTTCTTTTTACTCTCATCATATAGCTACAATGGAAGGGGGCTGCGTAGTTACT~~ 8040

D D E E L Y H V L L C L R A H G W T R N
~~GATGATGAAGAGCTGTATCATGTATTGTTGTGCCTTCGAGCTCATGGTTGGACAAGAAAT~~ 8100

L P K E N M V T G T K S D D I F E E S F
~~TTACCAAAAGAGAATATGGTTACAGGCACTAAGAGTGATGATATTTTCGAAGAGTCGTTT~~ 8160

K F V L P G Y N V R P L E M S G A I G I
~~AAGTTTGTTTTACCAGGATACAATGTTCGCCCACTTGAAATGAGTGGTGCTATTGGGATA~~ 8220

E Q L K K L P G F I S T R R S N A Q Y F
~~GAGCAACTTAAAAAGTTACCAGGTTTTATATCCACCAGACGTTCCAATGCACAATATTTT~~ 8280

V D K F K D H P F L D I Q K E V G E S S
~~GTAGATAAATTTAAAGATCATCCATTCCTTGATATACAAAAAGAAGTTGGTGAAAGTAGC~~ 8340

W F G F S F V I K E G A A I E R K S L V
~~TGGTTTGGTTTTTCCTTCGTTATAAAGGAGGGAGCTGCTATTGAGAGGAAGAGTTTAGTA~~ 8400

N N L I S A G I E C R P I V T G N F L K
~~AATAATCTGATCTCAGCAGGCATTGAATGCCGACCAATTGTTACTGGGAATTTTCTCAAA~~ 8460

N E R V L S Y F D Y S V H D T V A N A E
~~AATGAACGTGTTTTGAGTTATTTTGATTACTCTGTACATGATACGGTAGCAAATGCCGAA~~ 8520

Y I D K N G F F V G N H Q I P L F N E I
~~TATATAGATAAGAATGGTTTTTTTGTCGGAAACCACCAGATACCTTTGTTTAATGAAATA~~ 8580

End of orf7

D Y L R K V L K *

~~GATTATCTACGAAAAGTATTAAAATAACTAACGAGGCACTCTATTTCGAATAGAGTGCCT~~ 8640

Start of orf8

M V L T V K K I L A F G Y S K V L P
~~TTAAGATGGTATTAACAGTGAAAAAAATTTTAGCGTTTGGCTATTCTAAAGTACTACCAC~~ 8700

P V I E Q F V N P I C I F I I T P L I L
~~CGGTTATTGAACAGTTTGTCAATCCAATTTGCATCTTCATTATCACACCACTAATACTCA~~ 8760

N H L G K Q S Y G N W I L L I T I V S F
~~ACCACCTGGGTAAGCAAAGCTATGGTAATTGGATTTTATTAATTACTATTGTATCTTTTT~~ 8820

S Q L I C G G C S A W I A K I I A E Q R
~~CTCAGTTAATATGTGGAGGATGTTCCGCATGGATTGCAAAAATCATTGCAGAACAGAGAA~~ 8880

I L S D L S K K N A L R Q I S Y N F S I
~~TTCTTAGTGATTTATCAAAAAAAAATGCTTTACGTCAAATTTCCTATAATTTTTCAATTG~~ 8940

V I I A F A V L I S F L I L S I C F F D
~~TTATTATCGCATTTGCGGTATTGATTTCTTTTCTTATATTAAGTATTTGTTTCTTCGATG~~ 9000

V A R N N S S F L F A I I I C G F F Q E
~~TTGCGAGGAATAATTCTTCATTCTTATTCGCGATTATTATTTGTGGTTTTTTTCAGGAAG~~ 9060

V D N L F S G A L K G F E K F N V S C F
~~TTGATAATTTATTTAGTGGTGCGCTAAAAGGTTTTGAAAAATTTAATGTATCATGTTTTT~~ 9120

F E V I T R V L W A S I V I Y G I Y G N
~~TTGAAGTAATTACAAGAGTGCTCTGGGCTTCTATAGTAATATATGGCATTTACGGAAATG~~ 9180

A L L Y F T C L A F T I K G M L K Y I L
~~CACTCTTATATTTTACATGTTTAGCCTTTACCATTAAAGGTATGCTAAAATATATTCTTG~~ 9240

V C L N I T G C F I N P N F N R V G I V
~~TATGTCTGAATATTACCGGTTGTTTCATCAATCCTAATTTTAATAGAGTTGGGATTGTTA~~ 9300

N L L N E S K W M F L Q L T G G V S L S
~~ATTTGTTAAATGAGTCAAAATGGATGTTTCTTCAATTAACTGGTGGCGTCTCACTTAGTT~~ 9360

L F D R L V I P L I L S V S K L A S Y V
~~TGTTTGATAGGCTCGTAATACCATTGATTTTATCTGTCAGTAAACTGGCTTCTTATGTCC~~ 9420

P C L Q L A Q L M F T L S A S A N Q I L
~~CTTGCCTTCAACTAGCTCAATTGATGTTCAGTCTTTCTGCGTCTGCAAATCAAATATTAC~~ 9480

L P M F A R M K A S N T F P S N C F F K
~~TACCAATGTTTGCTAGAATGAAAGCATCTAACACATTTCCCTCTAATTGTTTTTTTAAAA~~ 9540

I L L V S L I S V L P C L A L F F F G R
~~TTCTGCTTGTATCACTAATTTCTGTTTTGCCTTGTCTTGCGTTATTCTTTTTTGGTCGTG~~ 9600

D I L S I W I N P T F A T E N Y K L M Q
~~ATATATTATCAATATGGATAAACCCTACATTTGCAACTGAAAATTATAAATTAATGCAAA~~ 9660

I L A I S Y I L L S M M T S F H F L L L
~~TTTTAGCTATAAGTTACATTTTATTGTCAATGATGACATCTTTTCATTTCTTGTTATTAG~~ 9720

G I G K S K L V A N L N L V A G L A L A
~~GAATTGGTAAATCTAAGCTTGTTGCAAATTTAAATCTGGTTGCAGGGCTCGCACTTGCTG~~ 9780

A S T L I A A H Y G L Y A I S M V K I I
~~CTTCAACGTTAATCGCAGCTCATTATGGCCTTTATGCAATATCTATGGTAAAAATAATAT~~ 9840

Y P A F Q F Y Y L Y V A F V Y F N R A K
~~ATCCGGCTTTTCAATTTTATTACCTTTATGTAGCTTTTGTCTATTTTAATAGAGCGAAAA~~ 9900

Start of orf9, End of orf8

M S I D L L F S I T E I A I V F S C T I
N V Y *
~~ATGTCTATTGATTTACTTTTTTCAATTACTGAAATCGCAATTGTTTTTTCTTGCACTATT~~ 9960

Y I F T Q C L L M R R I Y L D K S I L I
~~TACATATTTACTCAATGTTTG~~TTAATGCGGAGGATCTATTTAGATAAAAGTATTTTAATT 10020

L L C L L F F L V I I Q L P E L N V N G
CTTTTATGCTTGCTCTTTTTTTTAGTAATCATTCAACTTCCTGAGCTTAATGTAAACGGT 10080

```
 L  V  D  S  L  K  L  S  L  P  L  L  M  V  F  I  A  F  Q  K
TTGGTCGATTCTTTAAAGTTATCACTGCCTTTATTGATGGTCTTTATCGCTTTTCAAAAA   10140

 P  K  L  C  L  W  V  I  I  A  L  L  F  L  N  S  A  F  N  F
CCGAAATTATGCTTGTGGGTTATTATTGCATTGTTGTTTTTGAACTCTGCATTTAATTTT   10200

 L  Y  L  K  T  F  D  K  F  S  S  F  P  F  T  F  F  I  L  L
TTATATTTAAAGACATTCGATAAGTTTAGCTCATTTCCTTTTACTTTTTTTATATTGCTG   10260

 F  Y  L  F  R  L  G  I  G  N  L  P  V  Y  K  N  K  K  F  Y
TTTTACTTGTTTAGATTGGGAATTGGTAATTTACCGGTTTATAAAAATAAAAAATTTTAC   10320

 A  L  I  F  L  F  I  L  I  D  I  M  Q  S  L  L  I  N  Y  R
GCGTTGATTTTTCTCTTTATATTAATAGACATAATGCAGTCATTGTTAATAAATTATAGG   10380

 G  Q  I  L  Y  S  V  I  C  I  L  I  L  V  F  K  V  N  L  R
GGGCAGATTTTATATTCCGTAATTTGCATCCTGATACTTGTGTTTAAAGTTAATTTAAGA   10440

 K  K  I  P  Y  F  F  L  M  L  P  V  L  Y  V  I  I  M  A  Y
AAAAAGATTCCATACTTTTTTTTAATGCTGCCAGTTTTATATGTAATTATTATGGCTTAT   10500

 I  G  F  N  Y  F  N  K  G  V  T  F  F  E  P  T  A  S  N  I
ATTGGTTTTAATTATTTCAATAAAGGCGTAACTTTTTTTGAACCTACAGCAAGTAATATT   10560

 E  R  T  G  M  I  Y  Y  L  V  S  Q  L  G  D  Y  I  F  H  G
GAACGTACGGGGATGATATATTATTTGGTTTCACAGCTTGGTGATTATATATTCCATGGT   10620

 M  G  T  L  N  F  L  N  N  G  G  Q  Y  K  T  L  Y  G  L  P
ATGGGGACATTAAATTTCTTAAATAACGGCGGACAATATAAGACGTTATATGGACTTCCA   10680

 S  L  I  P  N  D  P  H  D  F  L  L  R  F  F  I  S  I  G  V
TCATTAATTCCTAATGACCCTCATGATTTTTTATTACGGTTCTTTATAAGTATTGGTGTG   10740

 I  G  A  L  V  Y  H  S  I  F  F  V  F  F  R  R  I  S  F  L
ATAGGAGCATTGGTTTATCATTCTATATTTTTTGTTTTTTTTAGGAGAATATCTTTCTTA   10800

 L  Y  E  R  N  A  P  F  I  V  V  S  C  L  L  L  L  Q  V  V
TTATATGAGAGAAATGCTCCTTTCATTGTTGTAAGTTGTTTGTTACTGTTACAAGTTGTG   10860

 L  I  Y  T  L  N  P  F  D  A  F  N  R  L  I  C  G  L  T  V
TTAATTTATACATTAAACCCTTTTGATGCTTTTAATCGATTGATTTGCGGGCTTACAGTT   10920
```

Start of orf10 **End of orf9**

```
 G  V  V  Y  G  F  A  K  I  R  *
             M  D  L  Q  K  L  D  K  Y  T  C  N  G  N  L  D  A
GGAGTTGTTTATGGATTTGCAAAAATTAGATAAGTATACCTGTAATGGAAATTTAGACGC   10980

 P  L  V  S  I  I  I  A  T  Y  N  S  E  L  D  I  A  K  C  L
TCCACTTGTTTCAATAATCATTGCAACTTATAATTCTGAACTTGATATAGCTAAGTGTTT   11040

 Q  S  V  T  N  Q  S  Y  K  N  I  E  I  I  I  M  D  G  G  S
GCAATCGGTAACTAATCAATCTTATAAGAATATTGAAATCATAATAATGGATGGAGGATC   11100

 S  D  K  T  L  D  I  A  K  S  F  K  D  D  R  I  K  I  V  S
TTCTGATAAAACGCTTGATATTGCAAAATCGTTTAAAGACGACCGAATAAAAATAGTTTC   11160

 E  K  D  R  G  I  Y  D  A  W  N  K  A  V  D  L  S  I  G  D
AGAGAAAGATCGTGGAATTTATGATGCCTGGAATAAAGCAGTTGATTTATCCATTGGTGA   11220

 W  V  A  F  I  G  S  D  D  V  Y  Y  H  T  D  A  I  A  S  L
TTGGGTAGCATTTATTGGTTCAGATGATGTTTACTATCATACAGATGCAATTGCTTCATT   11280

 M  K  G  V  M  V  S  N  G  A  P  V  V  Y  G  R  T  A  H  E
GATGAAGGGGGTTATGGTATCTAATGGCGCCCCTGTGGTTTATGGGAGGACAGCGCACGA   11340
```

Figure 5

```
 G  P  D  R  N  I  S  G  F  S  G  S  E  W  Y  N  L  T  G  F
AGGTCCCGATAGGAACATATCTGGATTTTCAGGCAGTGAATGGTACAACCTAACAGGATT   11400

 K  F  N  Y  Y  K  C  N  L  P  L  P  I  M  S  A  I  Y  S  R
TAAGTTTAATTATTACAAATGTAATTTACCATTGCCCATTATGAGCGCAATATATTCTCG   11460

 D  F  F  R  N  E  R  F  D  I  K  L  K  I  V  A  D  A  D  W
TGATTTCTTCAGAAACGAACGTTTGATATTAAATTAAAAATTGTTGCTGACGCTGATTG   11520

 F  L  R  C  F  I  K  W  S  K  E  K  S  P  Y  F  I  N  D  T
GTTTCTGAGATGTTTCATCAAATGGAGTAAAGAGAAGTCACCTTATTTTATTAATGACAC   11580

 T  P  I  V  R  M  G  Y  G  G  V  S  T  D  I  S  S  Q  V  K
GACCCCTATTGTTAGAATGGGATATGGTGGGGTTTCGACTGATATTTCTTCTCAAGTTAA   11640

 T  T  L  E  S  F  I  V  R  K  K  N  N  I  S  C  L  N  I  Q
AACTACGCTAGAAAGTTTCATTGTACGCAAAAAGAATAATATATCCTGTTTAAACATACA   11700

 L  I  L  R  Y  A  K  I  L  V  M  V  A  I  K  N  I  F  G  N
GCTGATTCTTAGATATGCTAAAATTCTGGTGATGGTAGCGATCAAAAATATTTTTGGCAA   11760

 N  V  Y  K  L  M  H  N  G  Y  H  S  L  K  K  I  K  N  K  I
TAATGTTTATAAATTAATGCATAACGGGTATCATTCCCTAAAGAAAATCAAGAATAAAAT   11820
```

Start of orf11, End of orf10

```
 M  K  I  V  Y  I  I  T  G  L  T  C  G  G  A  E  H  L  M  T
 *
ATGAAGATTGTTTATATAATAACCGGGCTTACTTGTGGTGGAGCCGAACACCTTATGACG   11880

 Q  L  A  D  Q  M  F  I  R  G  H  D  V  N  I  I  C  L  T  G
CAGTTAGCAGACCAAATGTTTATACGCGGGCATGATGTTAATATTATTTGTCTAACTGGT   11940

 I  S  E  V  K  P  T  Q  N  I  N  I  H  Y  V  N  M  D  K  N
ATATCTGAGGTAAAGCCAACACAAAATATTAATATTCATTATGTTAATATGGATAAAAAT   12000

 F  R  S  F  F  R  A  L  F  Q  V  K  K  I  I  V  A  L  K  P
TTTAGAAGCTTTTTTAGAGCTTTATTTCAAGTAAAAAAAATAATTGTCGCCTTAAAGCCA   12060

 D  I  I  H  S  H  M  F  H  A  N  I  F  S  R  F  I  R  M  L
GATATAATACATAGTCATATGTTTCATGCTAATATTTTTAGTCGTTTTATTAGGATGCTG   12120

 I  P  A  V  P  L  I  C  T  A  H  N  K  N  E  G  G  N  A  R
ATTCCAGCGGTGCCCCTGATATGTACCGCACACAACAAAAATGAAGGTGGCAATGCAAGG   12180

 M  F  C  Y  R  L  S  D  F  L  A  S  I  T  T  N  V  S  K  E
ATGTTTTGTTATCGACTGAGTGATTTTTTAGCTTCTATTACTACAAATGTAAGTAAAGAG   12240

 A  V  Q  E  F  I  A  R  K  A  T  P  K  N  K  I  V  E  I  P
GCTGTTCAAGAGTTTATAGCAAGAAAGGCTACACCTAAAAATAAAATAGTAGAGATTCCG   12300

 N  F  I  N  T  N  K  F  D  F  D  I  N  V  R  K  K  T  R  D
AATTTTATTAATACAAATAAATTTGATTTTGATATTAATGTCAGAAAGAAAACGCGAGAT   12360

 A  F  N  L  K  D  S  T  A  V  L  L  A  V  G  R  L  V  E  A
GCTTTTAATTTGAAAGACAGTACAGCAGTACTGCTCGCAGTAGGAAGACTTGTTGAAGCA   12420

 K  D  Y  P  N  L  L  N  A  I  N  H  L  I  L  S  K  T  S  N
AAAGACTATCCGAACTTATTAAATGCAATAAATCATTTGATTCTTTCAAAAACATCAAAT   12480

 C  N  D  F  I  L  L  I  A  G  D  G  A  L  R  N  K  L  L  D
TGTAATGATTTTATTTTGCTTATTGCTGGCGATGGCGCATTAAGAAATAAATTATTGGAT   12540

 L  V  C  Q  L  N  L  V  D  K  V  F  F  L  G  Q  R  S  D  I
TTGGTTTGTCAATTGAATCTTGTGGATAAAGTTTTCTTCTTGGGGCAAAGAAGTGATATT   12600
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 K  E  L  M  C  A  A  D  L  F  V  L  S  S  E  W  E  G  F  G
AAAGAATTAATGTGTGCTGCAGATCTTTTTGTTTTGAGTTCTGAGTGGGAAGGTTTTGGT   12660

 L  V  V  A  E  A  M  A  C  E  R  P  V  V  A  T  D  S  G  G
CTCGTTGTTGCAGAAGCTATGGCGTGTGAACGTCCCGTTGTTGCTACCGATTCTGGTGGA   12720

 V  K  E  V  V  G  P  H  N  D  V  I  P  V  S  N  H  I  L  L
GTTAAAGAAGTCGTTGGACCTCATAATGATGTTATCCCTGTCAGTAATCATATTCTGTTG   12780

 A  E  K  I  A  E  T  L  K  I  D  D  N  A  R  K  I  I  G  M
GCAGAGAAAATCGCTGAGACACTTAAAATAGATGATAACGCAAGAAAAATAATAGGTATG   12840

 K  N  R  E  Y  I  V  S  N  F  S  I  K  T  I  V  S  E  W  E
AAAAATAGAGAATATATTGTTTCCAATTTTTCAATTAAAACGATAGTGAGTGAGTGGGAG   12900

                                              End of orf11
 R  L  Y  F  K  Y  S  K  R  N  N  I  I  D  *
CGCTTATATTTTAAATATTCCAAGCGTAATAATATAATTGAT TGAAAATATAAGTTTGTA   12960

CTCTGGATGCAATAGTTTCTCTATGCTGTTTTTTACTGGCTCCGTATTTTTACTTATAG   13020

CTGGATTTTGTTATATATCAGTATTAATCTGTCTCAACTTCATCTAGACTACATTCAAGC   13080

                                               Start of gnd
                                               M  S  K  Q  Q  I
CGCGCATGCGTCGCGCGGTGACTACACCTGACAGGAGTATGTAATGTCCAAGCAACAGAT   13140

  G  V  V  G  M  A  V  M  G  R  N  L  A  L  N  I  E  S  R  G
CGGCGTCGTCGGTATGGCAGTGATGGGGCGCAACCTGGCGCTCAACATCGAAAGCCGCGG   13200

  Y  T  V  S  I  F  N  R  S  R  E  K  T  E  E  V  V  A  E  N
TTATACCGTCTCCATCTTCAACCGCTCCCGCGAGAAAACTGAAGAAGTTGTTGCCGAGAA   13260

  P  D  K  K  L  V  P  Y  Y  T  V  K  E  F  V  E  S  L  E  T
CCCGGATAAGAAACTGGTTCCTTATTACACGGTGAAAGAGTTCGTCGAGTCTCTTGAAAC   13320

  P  R  R  I  L  L  M  V  K  A  G  A  G  T  D  A  A  I  D  S
CCCACGTCGTATCCTGTTAATGGTAAAAGCAGGGGCGGGAACTGATGCTGCTATCGATTC   13380

  L  K  P  Y  L  D  K  G  D  I  I  I  D  G  G  N  T  F  F  Q
CCTGAAGCCGTATCTGGATAAAGGCGACATCATTATTGATGGTGGCAACACCTTCTTCCA   13440

  D  T  I  R  R  N  R  E  L  S  A  E  G  F  N  F  I  G  T  G
GGACACTATCCGTCGTAACCGTGAACTGTCCGCGGAAGGCTTTAACTTCATCGGTACCGG   13500

  V  S  G  G  E  E  G  A  L  K  G  P  S  I  M  P  G  G  Q  K
CGTGTCCGGCGGTGAAGAGGGCGCCCTGAAAGGCCCATCTATCATGCCAGGTGGCCAGAA   13560

  E  A  Y  E  L  V  A  P  I  L  T  K  I  A  A  V  A  E  D  G
AGAAGCGTATGAGCTGGTTGCGCCTATCCTGACCAAGATTGCTGCGGTTGCTGAAGATGG   13620

  E  P  C  I  T  Y  I  G  A  D  G  A  G  H  Y  V  K  M  V  H
CGAACCATGTATAACTTACATCGGTGCTGACGGTGCGGGTCACTACGTGAAGATGGTGCA   13680

  N  G  I  E  Y  G  D  M  Q  L  I  A  E  A  Y  S  L  L  K  G
CAACGGTATCGAATATGGCGATATGCAGCTGATTGCTGAAGCCTATTCTCTGCTTAAAGG   13740

  G  L  N  L  S  N  E  E  L  A  T  T  F  T  E  W  N  E  G  E
CGGCCTTAATCTGTCTAACGAAGAGCTGGCAACCACTTTTACCGAGTGGAATGAAGGCGA   13800

  L  S  S  Y  L  I  D  I  T  K  D  I  F  T  K  K  D  E  E  G
GCTAAGTAGCTACCTGATTGACATCACCAAAGACATCTTCACCAAAAAAGATGAAGAGGG   13860
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 K  Y  L  V  D  V  I  L  D  E  A  A  N  K  G  T  G  K  W  T
TAAATACCTGGTTGATGTGATCCTGGACGAAGCTGCGAACAAAGGCACCGGTAAATGGAC   13920

 S  Q  S  S  L  D  L  G  E  P  L  S  L  I  T  E  S  V  F  A
CAGCCAGAGCTCTCTGGATCTGGGTGAACCGCTGTCGCTGATCACCGAATCCGTATTCGC   13980

 R  Y  I  S  S  L  K  D  Q  R  I  A  A  S  K  V  L  S  G  P
TCGCTACATCTCTTCTCTGAAAGACCAGCGCATTGCGGCATCTAAAGTGCTGTCTGGTCC   14040

 Q  A  K  L  A  G  D  K  A  E  F  V  E  K  V  R  R  A  L  Y
GCAGGCTAAACTGGCTGGTGATAAAGCAGAGTTCGTTGAGAAAGTCCGTCGCGCGCTGTA   14100

 L  G  K  I  V  S  Y  A  Q  G  F  S  Q  L  R  A  A  S  D  E
CCTGGGTAAAATCGTCTCTTATGCCCAAGGCTTCTCTCAACTGCGTGCCGCGTCTGACGA   14160

 Y  N  W  D  L  N  Y  G  E  I  A  K  I  F  R  A  G  C  I  I
ATACAACTGGGATCTGAACTACGGCGAAATCGCGAAGATCTTCCGCGCGGGCTGCATCAT   14220

 R  A  Q  F  L  Q  K  I  T  D  A  Y  A  E  N  K  G  I  A  N
TCGTGCGCAGTTCCTGCAGAAAATTACTGACGCGTATGCTGAAAACAAAGGCATTGCTAA   14280

 L  L  L  A  P  Y  F  K  N  I  A  D  E  Y  Q  Q  A  L  R  D
CCTGTTGCTGGCTCCGTACTTCAAAAATATCGCTGATGAATATCAGCAAGCGCTGCGTGA   14340

 V  V  A  Y  A  V  Q  N  G  I  P  V  P  T  F  S  A  A  V  A
TGTAGTGGCTTATGCTGTGCAGAACGGTATTCCGGTACCGACCTTCTCTGCAGCGGTAGC   14400

 Y  Y  D  S  Y  R  S  A  V  L  P  A  N  L  I  Q  A  Q  R  D
CTACTACGACAGCTACCGTTCTGCGGTACTGCCGGCTAATCTGATTCAGGCACAGCGTGA   14460

 Y  F  G  A  H  T  Y  K  R  T  D  K  E  G  V  F  H  T  G
TTACTTCGGTGCGCACACGTATAAACGCACTGATAAAGAAGGTGTGTTCCACACCG   14516
```

Figure 5(i)

GTAACCAAGGGCGGTACGTGCATAAATTTTAATGCTTATCAAAACTATTAGCATTAAAAA 60

Start of orf1

M N K E T V S I I M P V Y N
TATATAAGAAATTCTCAAATGAAGAAAGAAACCGTTTCAATAATTATGCCCGTTTACAAT 120

G A K T I I S S V E S I I H Q S Y Q D F
GGGGCCAAAACTATAATCTCATCAGTAGAATCAATTATACATCAATCTTATCAAGATTTT 180

V L Y I I D D C S T D D T F S L I N S R
GTTTTGTATATCATTGACGATTGTAGCACCGATGATACATTTTCATTAATCAACAGTCGA 240

Y K N N Q K I R I L R N K T N L G V A E
TACAAAAACAATCAGAAAATAAGAATATTGCGTAACAAGACAAATTTAGGTGTTGCAGAA 300

S R N Y G I E M A T G K Y I S F C D A D
AGTCGAAATTATGGAATAGAAATGGCCACGGGGAAATATATTTCTTTTTGTGATGCGGAT 360

D L W H E K K L E R Q I E V L N N E C V
GATTTGTGGCACGAGAAAAAATTAGAGCGTCAAATCGAAGTGTTAAATAATGAATGTGTA 420

D V V C S N Y Y V I D N N R N I V G E V
GATGTGGTATGTTCTAATTATTATGTTATAGATAACAATAGAAATATTGTTGGCGAAGTT 480

N A P H V I N Y R K M L M K N Y I G N L
AATGCTCCTCATGTGATAAATTATAGAAAAATGCTCATGAAAAACTACATAGGGAATTTG 540

T G I Y N A N K L G K F Y Q K K I G H E
ACAGGAATCTATAATGCCAACAAATTGGGTAAGTTTTATCAAAAAAAGATTGGTCACGAG 600

D Y L M W L E I I N K T N G A I C I Q D
GATTATTTGATGTGGCTGGAAATAATTAATAAAACAAATGGTGCTATTTGTATTCAAGAT 660

N L A Y Y M R S N N S L S G N K I K A A
AATCTGGCGTATTACATGCGTTCAAATAATTCACTATCGGGTAATAAAATTAAAGCTGCA 720

K W T W S I Y R E H L H L S F P K T L Y
AAATGGACATGGAGTATATATAGAGAACATTTACATTTGTCCTTTCCAAAAACATTATAT 780

Y F L L Y A S N G V M K K I T H S L L R
TATTTTTTATTATATGCTTCAAATGGAGTCATGAAAAAAATAACACATTCACTATTAAGG 840

Start of orf2, End of orf1

R K E T K K *
V K S A A K L I F L F L F T
AGAAAGGAGACTAAAAAGTGAAGTCAGCGGCTAAGTTGATTTTTTTATTCCTATTTACAC 900

L Y S L Q L Y G V I I D D R I T N F D T
TTTATAGTCTCCAGTTGTATGGGGTTATCATAGATGATCGTATAACAAATTTTGATACAA 960

K V L T S I I I I F Q I F F V L L F Y L
AGGTATTAACTAGTATTATAATTATATTTCAGATTTTTTTTGTTTTATTATTTTATCTAA 1020

T I I N E R K Q Q K K F I V N W E L K L
CGATTATAAATGAAAGAAAACAGCAGAAAAAAATTTATCGTGAACTGGGAGCTAAAGTTAA 1080

I L V F L F V T I E I A A V V L F L K E
TACTCGTTTTCCTTTTTGTGACTATAGAAATTGCTGCTGTAGTTTTATTTCTTAAAGAAG 1140

G I P I F D D D P G G A K L R I A E G N
GTATTCCTATATTTGATGATGATCCAGGGGGGGCTAAACTTAGAATAGCTGAAGGTAATG 1200

Figure 6 (a)

```
G  L  Y  I  R  Y  I  K  Y  F  G  N  I  V  V  F  A  L  I  I
GACTTTACATTAGATATATTAAGTATTTTGGTAATATAGTTGTGTTTGCATTAATTATTC   1260

L  Y  D  E  H  K  F  K  Q  R  T  I  I  F  V  Y  F  T  T  I
TTTATGATGAGCATAAATTCAAACAGAGGACCATCATATTTGTATATTTTACAACGATTG   1320

A  L  F  G  Y  R  S  E  L  V  L  L  I  L  Q  Y  I  L  I  T
CTTTATTTGGTTATCGTTCTGAATTGGTGTTGCTCATTCTTCAATATATATTGATTACCA   1380

N  I  L  S  K  D  N  R  N  P  K  I  K  R  I  I  G  Y  F  L
ATATCCTGTCAAAGGATAACCGTAATCCTAAAATAAAAAGAATAATAGGGTATTTTTTAT   1440

L  V  G  V  V  C  S  L  F  Y  L  S  L  G  Q  D  G  E  Q  N
TGGTAGGGGTTGTATGCTCGTTGTTTTATCTAAGTTTAGGACAAGACGGAGAACAAAATG   1500

D  S  Y  N  N  M  L  R  I  I  N  R  L  T  I  E  Q  V  E  G
ACTCATATAATAATATGTTAAGGATAATTAATAGGTTAACAATAGAGCAAGTTGAAGGTG   1560

V  P  Y  V  V  S  E  S  I  K  N  D  F  F  P  T  P  E  L  E
TTCCATATGTTGTTTCTGAATCTATTAAGAACGATTTCTTTCCGACACCAGAGTTAGAAA   1620

K  E  L  K  A  I  I  N  R  I  Q  G  I  K  H  Q  D  L  F  Y
AGGAATTAAAAGCAATAATAAATAGAATACAGGGAATAAAGCATCAAGACTTATTTTATG   1680

G  E  R  L  H  K  Q  V  F  G  D  M  G  A  N  F  L  S  V  T
GAGAACGGTTACATAAACAAGTATTTGGAGACATGGGAGCAAATTTTTTATCAGTTACTA   1740

T  Y  G  A  E  L  L  V  F  F  G  F  L  C  V  F  I  I  P  L
CGTATGGAGCAGAACTGTTAGTTTTTTTTGGTTTTCTCTGTGTATTCATTATCCCTTTAG   1800

G  I  Y  I  P  F  Y  L  L  K  R  M  K  K  T  H  S  S  I  N
GGATATATATACCTTTTTATCTTTTAAAGAGAATGAAAAAAACCCATAGCTCGATAAATT   1860

C  A  F  Y  S  Y  I  I  M  I  L  L  Q  Y  L  V  A  G  N  A
GCGCATTCTATTCATATATCATTATGATTTTATTGCAATACTTAGTGGCTGGGAATGCAT   1920

S  A  F  F  F  G  P  F  L  S  V  L  I  M  C  T  P  L  I  L
CGGCCTTCTTTTTTGGTCCTTTTCTCTCCGTATTGATAATGTGTACTCCTCTGATCTTAT   1980

                                      Start of orf3
                                      M  K  I  S  V  I  T  V  T  Y
L  H  D  T  L  K  R  L  S  R  N  E  N  I  S  Y  N  C  D  L
TGCATGATACGTTAAAGAGATTATCACGAAATGAAAATATCAGTTATAACTGTGACTTAT   2040

  End of orf2
 N  N  A  E  G  L  E  K  T  L  S  S  L  S  I  L  K  I  K  P
 *
AATAATGCTGAAGGGTTAGAAAAAACTTTAAGTAGTTTATCAATTTTAAAAATAAAACCT   2100

 F  E  I  I  I  V  D  G  G  S  T  D  G  T  N  R  V  I  S  R
TTTGAGATTATTATAGTTGATGGCGGCTCTACAGATGGAACGAATCGTGTCATTAGTAGA   2160

 F  T  S  M  N  I  T  H  V  Y  E  K  D  E  G  I  Y  D  A  M
TTTACTAGTATGAATATTACACATGTTTATGAAAAAGATGAAGGGATATATGATGCGATG   2220

 N  K  G  R  M  L  A  K  G  D  L  I  H  Y  L  N  A  G  D  S
AATAAGGGCCGAATGTTGGCCAAAGGCGACTTAATACATTATTTAAACGCCGGCGATAGC   2280

 V  I  G  D  I  Y  K  N  I  K  E  P  C  L  I  K  V  G  L  F
GTAATTGGAGATATATATAAAAATATCAAAGAGCCATGTTTGATTAAAGTTGGCCTTTTC   2340

 E  N  D  K  L  L  G  F  S  S  I  T  H  S  N  T  G  Y  C  H
GAAAATGATAAACTTCTGGGATTTTCTTCTATAACCCATTCAAATACAGGGTATTGTCAT   2400
```

```
 Q  G  V  I  F  P  K  N  H  S  E  Y  D  L  R  Y  K  I  C  A
CAAGGGGTGATTTTCCCAAAGAATCATTCAGAATATGATCTAAGGTATAAAATATGTGCT    2460

 D  Y  K  L  I  Q  E  V  F  P  E  G  L  R  S  L  S  L  I  T
GATTATAAGCTTATTCAAGAGGTGTTTCCTGAAGGGTTAAGATCTCTATCTTTGATTACT    2520

 S  G  Y  V  K  Y  D  M  G  G  V  S  S  K  K  R  I  L  R  D
TCGGGTTATGTAAAATATGATATGGGGGGAGTATCTTCAAAAAAAAGAATTTTAAGAGAT    2580

 K  E  L  A  K  I  M  F  E  K  N  K  K  N  L  I  K  F  I  P
AAAGAGCTTGCCAAAATTATGTTTGAAAAAAATAAAAAAAACCTTATTAAGTTTATTCCA    2640

 I  S  I  I  K  I  L  F  P  E  R  L  R  R  V  L  R  K  M  Q
ATTTCAATAATCAAAATTTTATTCCCTGAACGTTTAAGAAGAGTATTGCGGAAAATGCAA    2700

                                          Start of orf4   End of orf3
 Y  I  C  L  T  L  F  F  M  K  N  S  S  P  Y  D  N  E  *
                                                M  I  M  N  K  I
TATATTTGTCTAACTTTATTCTTCATGAAGAATAGTTCACCATATGATAATGAATAAAAT    2760

 K  K  I  L  K  F  C  T  L  K  K  Y  D  T  S  S  A  L  G  R
CAAAAAAATACTTAAATTTTGCACTTTAAAAAAATATGATACATCAAGTGCTTTAGGTAG    2820

 E  Q  E  R  Y  R  I  I  S  L  S  V  I  S  S  L  I  S  K  I
AGAACAGGAAAGGTACAGGATTATATCCTTGTCTGTTATTTCAAGTTTGATTAGTAAAAT    2880

 L  S  L  L  S  L  I  L  T  V  S  L  T  L  P  Y  L  G  Q  E
ACTCTCACTACTTTCTCTTATATTAACTGTAAGTTTAACTTTACCTTATTTAGGACAAGA    2940

 R  F  G  V  W  M  T  I  T  S  L  G  A  A  L  T  F  L  D  L
GAGATTTGGTGTATGGATGACTATTACCAGTCTTGGTGCTGCTCTGACATTTTTGGACTT    3000

 G  I  G  N  A  L  T  N  R  I  A  H  S  F  A  C  G  K  N  L
AGGTATAGGAAATGCATTAACAAACAGGATCGCACATTCATTTGCGTGTGGCAAAAATTT    3060

 K  M  S  R  Q  I  S  G  G  L  T  L  L  A  G  L  S  F  V  I
AAAGATGAGTCGGCAAATTAGTGGTGGGCTCACTTTGCTGGCTGGATTATCGTTTGTCAT    3120

 T  A  I  C  Y  I  T  S  G  M  I  D  W  Q  L  V  I  K  G  I
AACTGCAATATGCTATATTACTTCTGGCATGATTGATTGGCAACTAGTAATAAAAGGTAT    3180

 N  E  N  V  Y  A  E  L  Q  H  S  I  K  V  F  V  I  I  F  G
AAACGAGAATGTGTATGCAGAGTTACAACACTCAATTAAAGTCTTTGTAATCATATTTGG    3240

 L  G  I  Y  S  N  G  V  Q  K  V  Y  M  G  I  Q  K  A  Y  I
ACTTGGAATTTATTCAAATGGTGTGCAAAAAGTTTATATGGGAATACAAAAAGCCTATAT    3300

 S  N  I  V  N  A  I  F  I  L  L  S  I  I  T  L  V  I  S  S
AAGTAATATTGTTAATGCCATATTTATATTGTTATCTATTATTACTCTAGTAATATCGTC    3360

 K  L  H  A  G  L  P  V  L  I  V  S  T  L  G  I  Q  Y  I  S
GAAACTACATGCGGGACTACCAGTTTTAATTGTCAGCACTCTTGGTATTCAATACATATC    3420

 G  I  Y  L  T  I  N  L  I  I  K  R  L  I  K  F  T  K  V  N
GGGAATCTATTTAACAATTAATCTTATTATAAAGCGATTAATAAAGTTTACAAAAGTTAA    3480

 I  H  A  K  R  E  A  P  Y  L  I  L  N  G  F  F  F  F  I  L
CATACATGCTAAAAGAGAAGCTCCATATTTGATATTAAACGGTTTTTTCTTTTTTATTTT    3540

 Q  L  G  T  L  A  T  W  S  G  D  N  F  I  I  S  I  T  L  G
ACAGTTAGGCACTCTGGCAACATGGAGTGGTGATAACTTTATAATATCTATAACATTGGG    3600
```

V T Y V A V F S I T Q R L F Q I S T V P
TGTTACTTATGTTGCTGTTTTTAGCATTACACAGAGATTATTTCAAATATCTACGGTCCC 3660

L T I Y N I P L W A A Y A D A H A R N D
TCTTACGATTTATAACATCCCGTTATGGGCTGCTTATGCAGATGCTCATGCACGCAATGA 3720

T Q F I K K T L R T S L K I V G I S S F
TACTCAATTTATAAAAAAGACGCTCAGAACATCATTGAAAATAGTGGGTATTTCATCATT 3780

L L A F I L V V F G S E V V N I W T E G
CTTATTGGCCTTCATATTAGTAGTGTTCGGTAGTGAAGTCGTTAATATTTGGACAGAAGG 3840

K I Q V P R T F I I A Y A L W S V I D A
AAAGATTCAGGTACCTCGAACATTCATAATAGCTTATGCTTTATGGTCTGTTATTGATGC 3900

F S N T F A S F L N G L N I V K Q Q M L
TTTTTCGAATACATTTGCAAGCTTTTTAAATGGTTTGAACATAGTTAAACAACAAATGCT 3960

A V V T L I L I A I P A K Y I I V S H F
TGCTGTTGTAACATTGATATTGATCGCAATTCCAGCAAAATACATCATAGTTAGCCATTT 4020

G L T V M L Y C F I F I Y I V N Y F I W
T~~GGGTTAACTGTTATGTTGTACTGCTTCATTTTTATATATATTGTAAATTACTTTATATG~~ 4080

Start of orf5, End of orf4

M K M
Y K C S F K K H I D R Q L N I R G *
~~GTATAAATGTAGTTTTAAAAAACATATCGATAGACAGTTAAATATAAGAGGATGAAAATG~~ 4140

K Y I P V Y Q P S L T G K E K E Y V N E
~~AAATATATACCAGTTTACCAACCGTCATTGACAGGAAAAGAAAAAGAATATGTAAATGAA~~ 4200

C L D S T W I S S K G N Y I Q K F E N K
~~TGTCTGGACTCAACGTGGATTTCATCAAAAGGAAACTATATTCAGAAGTTTGAAAATAAA~~ 4260

F A E Q N H V Q Y A T T V S N G T V A L
~~TTTGCGGAACAAAACCATGTGCAATATGCAACTACTGTAAGTAATGGAACGGTTGCTCTT~~ 4320

H L A L L A L G I S E G D E V I V P T L
~~CATTTAGCTTTGTTAGCGTTAGGTATATCGGAAGGAGATGAAGTTATTGTTCCAACACTG~~ 4380

T Y I A S V N A I K Y T G A T P I F V D
~~ACATATATAGCATCAGTTAATGCTATAAAATACACAGGAGCCACCCCCATTTTCGTTGAT~~ 4440

S D N E T W Q M S V S D I E Q K I T N K
~~TCAGATAATGAAACTTGGCAAATGTCTGTTAGTGACATAGAACAAAAAATCACTAATAAA~~ 4500

T K A I M C V H L Y G H P C D M E Q I V
~~ACTAAAGCTATTATGTGTGTCCATTTATACGGACATCCATGTGATATGGAACAAATTGTA~~ 4560

E L A K S R N L F V I E D C A E A F G S
~~GAACTGGCCAAAAGTAGAAATTTGTTTGTAATTGAAGATTGCGCTGAAGCCTTTGGTTCT~~ 4620

K Y K G K Y V G T F G D I S T F S F F G
~~AAATATAAAGGTAAATATGTGGGAACATTTGGAGATATTTCTACTTTTAGCTTTTTTGGA~~ 4680

N K T I T T G E G G M V V T N D K T L Y
~~AATAAAACTATTACTACAGGTGAAGGTGGAATGGTTGTCACGAATGACAAAACACTTTAT~~ 4740

D R C L H F K G Q G L A V H R Q Y W H D
~~GACCGTTGTTTACATTTTAAAGGCCAAGGATTAGCTGTACATAGGCAATATTGGCATGAC~~ 4800

V I G Y N Y R M T N I C A A I G L A Q L
~~GTTATAGGCTACAATTATAGGATGACAAATATCTGCGCTGCTATAGGATTAGCCCAGTTA~~ 4860

E Q A D D F I S R K R E I A D I Y K K N
~~GAACAAGCTGATGATTTTATATCACGAAAACGTGAAATTGCTGATATTTATAAAAAAAAT~~ 4920

I N S L V Q V H K E S K D V F H T Y W M
~~ATCAACAGTCTTGTACAAGTCCACAAGGAAAGTAAAGATGTTTTTCACACTTATTGGATG~~ 4980

V S I L T R T A E E R E E L R N H L A D
~~GTCTCAATTCTAACTAGGACCGCAGAGGAAAGAGAGGAATTAAGGAATCACCTTGCAGAT~~ 5040

K L I E T R P V F Y P V H T M P M Y S E
~~AAACTCATCGAAACAAGGCCAGTTTTTTACCCTGTCCACACGATGCCAATGTACTCGGAA~~ 5100

K Y Q K H P I A E D L G W R G I N L P S
~~AAATATCAAAAGCACCCTATAGCTGAGGATCTTGGTTGGCGTGGAATTAATTTACCTAGT~~ 5160

F P S L S N E Q V I Y I C E S I N E F Y
~~TTCCCCAGCCTATCGAATGAGCAAGTTATTTATATTTGTGAATCTATTAACGAATTTTAT~~ 5220

End of orf5 **Start of orf6**
S D K * M K I A L N S D
~~AGTGATAAATAGCCTAAAATATTGTAAAGGTCATTCATGAAAATTGCGTTGAATTCAGAT~~ 5280

G F Y E W G G G I D F I K Y I L S I L E
~~GGATTTTACGAGTGGGGCGGTGGAATTG~~ATTTTATTAAATATATTCTGTCAATATTAGAA 5340

T K P E I C I D I L L P R N D I H S L I
ACGAAACCAGAAATATGTATCGATATTCTTTTACCGAGAAATGATATACATTCTCTTATA 5400

R E K A F P F K S I L K A I L K R E R P
AGAGAAAAAGCATTTCCTTTTAAAAGTATATTAAAAGCAATTTTAAAGAGGGAAAGGCCT 5460

R W I S L N R F N E Q Y Y R D A F T Q N
CGATGGATTTCATTAAATAGATTTAATGAGCAATACTATAGAGATGCCTTTACACAAAAT 5520

N I E T N L T F I K S K S S A F Y S Y F
AATATAGAGACGAATCTTACCTTTATTAAAAGTAAGAGCTCTGCCTTTTATTCATATTTT 5580

D S S D C D V I L P C M R V P S G N L N
GATAGTAGCGATTGTGATGTTATTCTTCCTTGCATGCGTGTTCCTTCGGGAAATTTGAAT 5640

K K A W I G Y I Y D F Q H C Y Y P S F F
AAAAAAGCATGGATTGGTTATATTTATGACTTTCAACACTGTTACTATCCTTCATTTTTT 5700

S K R E I D Q R N V F F K L M L N C A N
AGTAAGCGAGAAATAGATCAAAGGAATGTGTTTTTTAAATTGATGCTCAATTGCGCTAAC 5760

N I I V N A H S V I T D A N K Y V G N Y
AATATTATTGTTAATGCACATTCAGTTATTACCGATGCAAATAAATATGTTGGGAATTAT 5820

S A K L H S L P F S P C P Q L K W F A D
TCTGCAAAACTACATTCTCTTCCATTTAGTCCATGCCCTCAATTAAAATGGTTCGCTGAT 5880

Y S G N I A K Y N I D K D Y F I I C N Q
TACTCTGGTAATATTGCCAAATATAATATTGACAAGGATTATTTTATAATTTGCAATCAA 5940

F W K H K D H A T A F R A F K I Y T E Y
TTTTGGAAACATAAAGATCATGCAACTGCTTTTAGGGCATTTAAAATTTATACTGAATAT 6000

N P D V Y L V C T G A T Q D Y R F P G Y
AATCCTGATGTTTATTTAGTATGCACGGGAGCTACTCAAGATTATCGATTCCCTGGATAT 6060

F N E L M V L A K K L G I E S K I K I L
TTTAATGAATTGATGGTTTTGGCAAAAAAGCTCGGAATTGAATCGAAAATTAAGATATTA 6120

Figure 6

G H I P K L E Q I E L I K N C I A V I Q
GGGCATATACCTAAACTTGAACAAATTGAATTAATCAAAAATTGCATTGCTGTAATACAA 6180

P T L F E G G P G G G V T F D A I A L G
CCAACCTTATTTGAAGGCGGGCCTGGAGGGGGGGTAACATTTGACGCTATTGCATTAGGG 6240

K K V I L S D I D V N K E V N C G D V Y
AAAAAAGTTATACTATCTGACATAGATGTCAATAAAGAAGTTAATTGCGGTGATGTATAT 6300

F F Q A K N H Y S L N D A M V K A D E S
TTCTTTCAGGCAAAAAACCATTATTCATTAAATGACGCGATGGTAAAAGCTGATGAATCT 6360

K I F Y E P T T L I E L G L K R R N A C
AAAATTTTTTATGAACCTACAACTCTGATAGAATTGGGTCTCAAAAGACGCAATGCGTGT 6420

End of orf6
A D F L L D V V K Q E I E S R S *
GCAGATTTTCTTTTAGATGTTGTGAAACAAGAAATTGAATCCCGATCT *TAA*TATATTCAA 6480

Start of orf7
M T K V A L I T G V T G Q D G S Y
GAGGTATATA<u>ATG</u>ACTAAAGTCGCTCTTATTACAGGTGTAACTGGACAAGATGGATCTTA 6540

L A E F L L D K G Y E V H G I K R R A S
TCTAGCTGAGTTTTTGCTTGATAAAGGGTATGAAGTTCATGGTATCAAACGCCGAGCCTC 6600

S F N T E R I D H I Y Q D P H G S N P N
ATCTTTTAATACAGAACGCATAGACCATATTTATCAAGATCCACATGGTTCTAACCCAAA 6660

F H L H Y G D L T D S S N L T R I L K E
TTTTCACTTGCACTATGGAGATCTGACTGATTCATCTAACCTCACTAGAATTCTAAAGGA 6720

V Q P D E V Y N L A A M S H V A V S F E
GGTACAGCCAGATGAAGTATATAATTTAGCTGCTATGAGTCACGTAGCAGTTTCTTTTGA 6780

S P E Y T A D V D A I G T L R L L E A I
GTCTCCAGAATATACAGCCGATGTCGATGCAATTGGTACATTACGTTTACTGGAAGCAAT 6840

R F L G L E N K T R F Y Q A S T S E L Y
TCGCTTTTTAGGATTGGAAAACAAAACGCGTTTCTATCAAGCTTCAACCTCAGAATTATA 6900

G L V Q E I P Q K E S T P F Y P R S P Y
TGGACTTGTTCAGGAAATCCCTCAAAAAGAATCCACCCCTTTTTATCCTCGTTCCCCTTA 6960

A V A K L Y A Y W I T V N Y R E S Y G I
TGCAGTTGCAAAACTTTACGCATATTGGATCACGGTAAATTATCGAGAGTCATATGGTAT 7020

Y A C N G I L F N H E S P R R G E T F V
TTATGCATGTAATGGTATATTGTTCAATCATGAATCTCCACGCCGTGGAGAAACGTTTGT 7080

T R K I T R G L A N I A Q G L E S C L Y
AACAAGGAAAATTACTCGAGGACTTGCAAATATTGCACAAGGCTTGGAATCATGTTTGTA 7140

L G N M D S L R D W G H A K D Y V R M Q
TTTAGGGAATATGGATTCGTTACGAGATTGGGGACATGCAAAAGATTATGTTAGAATGCA 7200

W L M L Q Q E Q P E D F V I A T G V Q Y
ATGGTTGATGTTACAACAGGAGCAACCCGAAGATTTTGTGATTGCAACAGGAGTCCAATA 7260

S V R Q F V E M A A A Q L G I K M S F V
CTCAGTCCGTCAGTTTGTCGAAATGGCAGCAGCACAACTTGGTATTAAGATGAGCTTTGT 7320

Figure 6 f

```
 G  K  G  I  E  E  K  G  I  V  D  S  V  E  G  Q  D  A  P  G
TGGTAAAGGAATCGAAGAAAAAGGCATTGTAGATTCGGTTGAAGGACAGGATGCTCCAGG     7380

 V  K  P  G  D  V  I  V  A  V  D  P  R  Y  F  R  P  A  E  V
TGTGAAACCAGGTGATGTCATTGTTGCTGTTGATCCTCGTTATTTCCGACCAGCTGAAGT     7440

 D  T  L  L  G  D  P  S  K  A  N  L  K  L  G  W  R  P  E  I
TGATACTTTGCTTGGAGATCCGAGCAAAGCTAATCTCAAACTTGGTTGGAGACCAGAAAT     7500

 T  L  A  E  M  I  S  E  M  V  A  K  D  L  E  A  A  K  K  H
TACTCTTGCTGAAATGATTTCTGAAATGGTTGCCAAAGATCTTGAAGCCGCTAAAAAACA     7560


                                     Start of orf8, End of orf7
                                               M  M  M  N  K
 S  L  L  K  S  H  G  F  S  V  S  L  A  L  E  *
TTCTCTTTTAAAATCGCATGGTTTTTCTGTAAGCTTAGCTCTGGAATGATGATGAATAAG     7620

 Q  R  I  F  I  A  G  H  Q  G  M  V  G  S  A  I  T  R  R  L
CAACGTATTTTTATTGCTGGTCACCAAGGAATGGTTGGATCAGCTATTACCCGACGCCTC     7680

 K  Q  R  D  D  V  E  L  V  L  R  T  R  D  E  L  N  L  L  D
AAACAACGTGATGATGTTGAGTTGGTTTTACGTACTCGGGATGAATTGAACTTGTTGGAT     7740

 S  S  A  V  L  D  F  F  S  S  Q  K  I  D  Q  V  Y  L  A  A
AGTAGCGCTGTTTTGGATTTTTTTTCTTCACAGAAAATCGACCAGGTTTATTTGGCAGCA     7800

 A  K  V  G  G  I  L  A  N  S  S  Y  P  A  D  F  I  Y  E  N
GCAAAAGTCGGAGGTATTTTAGCTAACAGTTCTTATCCTGCCGATTTTATATATGAGAAT     7860

 I  M  I  E  A  N  V  I  H  A  A  H  K  N  N  V  N  K  L  L
ATAATGATAGAGGCGAATGTCATTCATGCTGCCCACAAAAATAATGTAAATAAACTGCTT     7920

 F  L  G  S  S  C  I  Y  P  K  L  A  H  Q  P  I  M  E  D  E
TTCCTCGGTTCGTCGTGTATTTATCCTAAGTTAGCACACCAACCGATTATGGAAGACGAA     7980

 L  L  Q  G  K  L  E  P  T  N  E  P  Y  A  I  A  K  I  A  G
TTATTACAAGGGAAACTTGAGCCAACAAATGAACCTTATGCTATCGCAAAAATTGCAGGT     8040

 I  K  L  C  E  S  Y  N  R  Q  F  G  R  D  Y  R  S  V  M  P
ATTAAATTATGTGAATCTTATAACCGTCAGTTTGGGCGTGATTACCGTTCAGTAATGCCA     8100

 T  N  L  Y  G  P  N  D  N  F  H  P  S  N  S  H  V  I  P  A
ACCAATCTTTATGGTCCAAATGACAATTTTCATCCAAGTAATTCTCATGTGATTCCGGCG     8160

 L  L  R  R  F  H  D  A  V  E  N  N  S  P  N  V  V  V  W  G
CTTTTGCGCCGCTTTCATGATGCTGTGGAAAACAATTCTCCGAATGTTGTTGTTTGGGGA     8220

 S  G  T  P  K  R  E  F  L  H  V  D  D  M  A  S  A  S  I  Y
AGTGGTACTCCAAAGCGTGAATTCTTACATGTAGATGATATGGCTTCTGCAAGCATTTAT     8280

 V  M  E  M  P  Y  D  I  W  Q  K  N  T  K  V  M  L  S  H  I
GTCATGGAGATGCCATACGATATATGGCAAAAAAATACTAAAGTAATGTTGTCTCATATC     8340

 N  I  G  T  G  I  D  C  T  I  C  E  L  A  E  T  I  A  K  V
AATATTGGAACAGGTATTGACTGCACGATTTGTGAGCTTGCGGAAACAATAGCAAAAGTT     8400

 V  G  Y  K  G  H  I  T  F  D  T  T  K  P  D  G  A  P  R  K
GTAGGTTATAAAGGGCATATTACGTTCGATACAACAAAGCCCGATGGAGCCCCTCGAAAA     8460

 L  L  D  V  T  L  L  H  Q  L  G  W  N  H  K  I  T  L  H  K
CTACTTGATGTAACGCTTCTTCATCAACTAGGTTGGAATCATAAAATTACCCTTCACAAG     8520
```

Figure 6

End of orf8

```
G  L  E  N  T  Y  N  W  F  L  E  N  Q  L  Q  Y  R  G  *
GGTCTTGAAAATACATACAACTGGTTTCTTGAAAACCAACTTCAATATCGGGGG TAATAA   8580
```

Start of orf9

```
M  F  L  H  S  Q  D  F  A  T  I  V  R  S  T  P  L  I  S  I
TGTTTTTACATTCCCAAGACTTTGCCACAATTGTAAGGTCTACTCCTCTTATTTCTATAG   8640

D  L  I  V  E  N  E  F  G  E  I  L  L  G  K  R  I  N  R  P
ATTTGATTGTGGAAAACGAGTTTGGCGAAATTTTGCTAGGAAAACGAATCAACCGCCCGG   8700

A  Q  G  Y  W  F  V  P  G  G  R  V  L  K  D  E  K  L  Q  T
CACAGGGCTATTGGTTCGTTCCTGGTGGTAGGGTGTTGAAAGATGAAAAATTGCAGACAG   8760

A  F  E  R  L  T  E  I  E  L  G  I  R  L  P  L  S  V  G  K
CCTTTGAACGATTGACAGAAATTGAACTAGGAATTCGTTTGCCTCTCTCTGTGGGTAAGT   8820

F  Y  G  I  W  Q  H  F  Y  E  D  N  S  M  G  G  D  F  S  T
TTTATGGTATCTGGCAGCACTTCTACGAAGACAATAGTATGGGGGGAGACTTTTCAACGC   8880

H  Y  I  V  I  A  F  L  L  K  L  Q  P  N  I  L  K  L  P  K
ATTATATAGTTATAGCATTCCTTCTTAAATTACAACCAAACATTTTGAAATTACCGAAGT   8940

S  Q  H  N  A  Y  C  W  L  S  R  A  K  L  I  N  D  D  D  V
CACAACATAATGCTTATTGCTGGCTATCGCGAGCAAAGCTGATAAATGATGACGATGTGC   9000

H  Y  N  C  R  A  Y  F  N  N  K  T  N  D  A  I  G  L  D  N
ATTATAATTGTCGCGCATATTTTAACAATAAAACAAATGATGCGATTGGCTTAGATAATA   9060
```

Start of orf10 **End of orf9**

```
           M  S  D  A  P  I  I  A  V  V  M  A  G  G  T  G  S
K  D  I  I  C  L  M  R  Q  *
AGGATATAATATGTCTGATGCGCCAA TAATTGCTGTAGTTATGGCCGGTGGTACAGGCAG   9120

 R  L  W  P  L  S  R  E  L  Y  P  K  Q  F  L  Q  L  S  G  D
TCGTCTTTGGCCACTTTCTCGTGAACTATATCCAAAGCAGTTTTTACAACTCTCTGGTGA   9180

 N  T  L  L  Q  T  T  L  L  R  L  S  G  L  S  C  Q  K  P  L
TAACACCTTGTTACAAACGACTTTGCTACGACTTTCAGGCCTATCATGTCAAAAACCATT   9240

 V  I  T  N  E  Q  H  R  F  V  V  A  E  Q  L  R  E  I  N  K
AGTGATAACAAATGAACAGCATCGCTTTGTTGTGGCTGAACAGTTAAGGGAAATAAATAA   9300

 L  N  G  N  I  I  L  E  P  C  G  R  N  T  A  P  A  I  A  I
ATTAAATGGTAATATTATTCTAGAACCATGCGGGCGAAATACTGCACCAGCAATAGCGAT   9360

 S  A  F  H  A  L  K  R  N  P  Q  E  D  P  L  L  L  V  L  A
ATCTGCGTTTCATGCGTTAAAACGTAATCCTCAGGAAGATCCATTGCTTCTAGTTCTTGC   9420

 A  D  H  V  I  A  K  E  S  V  F  C  D  A  I  K  N  A  T  P
GGCAGACCACGTTATAGCTAAAGAAAGTGTTTTCTGTGATGCTATTAAAAATGCAACTCC   9480

 I  A  N  Q  G  K  I  V  T  F  G  I  I  P  E  Y  A  E  T  G
CATCGCTAATCAAGGTAAAATTGTAACGTTTGGAATTATACCAGAATATGCTGAAACTGG   9540

 Y  G  Y  I  E  R  G  E  L  S  V  P  L  Q  G  H  E  N  T  G
TTATGGGTATATTGAGAGAGGTGAACTATCTGTACCGCTTCAAGGGCATGAAAATACTGG   9600

 F  Y  Y  V  N  K  F  V  E  K  P  N  R  E  T  A  E  L  Y  M
TTTTTATTATGTAAATAAGTTTGTCGAAAAGCCTAATCGTGAAACCGCAGAATTGTATAT   9660

 T  S  G  N  H  Y  W  N  S  G  I  F  M  F  K  A  S  V  Y  L
GACTTCTGGTAATCACTATTGGAATAGTGGAATATTCATGTTTAAGGCATCTGTTTATCT   9720
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 E  E  L  R  K  F  R  P  D  I  Y  N  V  C  E  Q  V  A  S  S
TGAGGAATTGAGAAAATTTAGACCTGACATTTACAATGTTTGTGAACAGGTTGCCTCATC   9780

 S  Y  I  D  L  D  F  I  R  L  S  K  E  Q  F  Q  D  C  P  A
CTCATACATTGATCTAGATTTTATTCGATTATCAAAAGAACAATTTCAAGATTGTCCTGC   9840

 E  S  I  D  F  A  V  M  E  K  T  E  K  C  V  V  C  P  V  D
TGAATCTATTGATTTTGCTGTAATGGAAAAAACAGAAAAATGTGTTGTATGCCCTGTTGA   9900

 I  G  W  S  D  V  G  S  W  Q  S  L  W  D  I  S  L  K  S  K
TATTGGTTGGAGTGACGTTGGATCTTGGCAATCGTTATGGGACATTAGTCTAAAATCGAA   9960

 T  G  D  V  C  K  G  D  I  L  T  Y  D  T  K  N  N  Y  I  Y
AACAGGAGATGTATGTAAAGGTGATATATTAACCTATGATACTAAGAATAATTATATCTA   10020

 S  E  S  A  L  V  A  A  I  G  I  E  D  M  V  I  V  Q  T  K
CTCTGAGTCAGCGTTGGTAGCCGCCATTGGAATTGAAGATATGGTTATCGTGCAAACTAA   10080

 D  A  V  L  V  S  K  K  S  D  V  Q  H  V  K  K  I  V  E  M
AGATGCCGTTCTTGTGTCTAAAAAGAGTGATGTACAGCATGTAAAAAAAATAGTCGAAAT   10140

 L  K  L  Q  Q  R  T  E  Y  I  S  H  R  E  V  F  R  P  W  G
GCTTAAATTGCAGCAACGTACAGAGTATATTAGTCATCGTGAAGTTTTCCGACCATGGGG   10200

 K  F  D  S  I  D  Q  G  E  R  Y  K  V  K  K  I  I  V  K  P
AAAATTTGATTCGATTGACCAAGGTGAGCGATACAAAGTCAAGAAAATTATTGTGAAACC   10260

 G  E  G  L  S  L  R  M  H  H  H  R  S  E  H  W  I  V  L  S
TGGTGAGGGGCTTTCTTTAAGGATGCATCACCATCGTTCTGAACATTGGATCGTGCTTTC   10320

 G  T  A  K  V  T  L  G  D  K  T  K  L  V  T  A  N  E  S  I
TGGTACAGCAAAAGTAACCCTTGGCGATAAAACTAAACTAGTCACCGCAAATGAATCGAT   10380

 Y  I  P  L  G  A  A  Y  S  L  E  N  P  G  I  I  P  L  N  L
ATACATTCCCCTTGGCGCAGCGTATAGTCTTGAGAATCCGGGCATAATCCCTCTTAATCT   10440

 I  E  V  S  S  G  D  Y  L  G  E  D  D  I  I  R  Q  K  E  R
TATTGAAGTCAGTTCAGGGGATTATTTGGGAGAGGATGATATTATAAGACAGAAAGAACG   10500

         End of orf10  Start of orf11
 Y  K  H  E  D  *     M  K  S  L  T  C  F  K  A  Y  D  I  R
TTACAAACATGAAGATTAACATATGAAATCTTTAACCTGCTTTAAAGCCTATGATATTCG   10560

 G  K  L  G  E  E  L  N  E  D  I  A  W  R  I  G  R  A  Y  G
CGGGAAATTAGGCGAAGAACTGAATGAAGATATTGCCTGGCGCATTGGGCGTGCCTATGG   10620

 E  F  L  K  P  K  T  I  V  L  G  G  D  V  R  L  T  S  E  A
CGAATTTCTCAAACCGAAAACCATTGTTTTAGGCGGTGATGTCCGCCTCACCAGCGAAGC   10680

 L  K  L  A  L  A  K  G  L  Q  D  A  G  V  D  V  L  D  I  G
GTTAAAACTGGCGCTTGCGAAAGGTTTACAGGATGCGGGCGTCGATGTGCTGGATATCGG   10740

 M  S  G  T  E  E  I  Y  F  A  T  F  H  L  G  V  D  G  G  I
TATGTCCGGCACCGAAGAGATCTATTTCGCCACGTTCCATCTCGGAGTGGATGGCGGCAT   10800

 E  V  T  A  S  H  N  P  M  D  Y  N  G  M  K  L  V  R  E  G
CGAAGTTACCGCCAGCCATAACCCGATGGATTACAACGGCATGAAGCTGGTGCGCGAAGG   10860

 A  R  P  I  S  G  D  T  G  L  R  D  V  Q  R  L  A  E  A  N
GGCTCGCCCGATCAGCGGTGATACCGGACTGCGCGATGTCCAGCGTCTGGCAGAAGCCAA   10920

 D  F  P  P  V  D  E  T  K  R  G  R  Y  Q  Q  I  N  L  R  D
TGACTTCCCTCCTGTCGATGAAACCAAACGTGGTCGCTATCAGCAAATCAATCTGCGTGA   10980
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 A  Y  V  D  H  L  F  G  Y  I  N  V  K  N  L  T  P  L  K  L
CGCTTACGTTGATCACCTGTTCGGTTATATCAACGTCAAAAACCTCACGCCGCTCAAGCT  11040

 V  I  N  S  G  N  G  A  A  G  P  V  V  D  A  I  E  A  R  F
GGTGATCAACTCCGGGAACGGCGCAGCGGGTCCGGTGGTGGACGCCATTGAAGCCCGATT  11100

 K  A  L  G  A  P  V  E  L  I  K  V  H  N  T  P  D  G  N  F
TAAAGCCCTCGGCGCACCGGTGGAATTAATCAAAGTACACAACACGCCGGACGGCAATTT  11160

 P  N  G  I  P  N  P  L  L  P  E  C  R  D  D  T  R  N  A  V
CCCCAACGGTATTCCTAACCCGCTGCTGCCGGAATGCCGCGACGACACCCGTAATGCGGT  11220

 I  K  H  G  A  D  M  G  I  A  F  D  G  D  F  D  R  C  F  L
CATCAAACACGGCGCGGATATGGGCATTGCCTTTGATGGCGATTTTGACCGCTGTTTCCT  11280

 F  D  E  K  G  Q  F  I  E  G  Y  Y  I  V  G  L  L  A  E  A
GTTTGACGAAAAAGGGCAGTTTATCGAGGGCTACTACATTGTCGGCCTGCTGGCAGAAGC  11340

 F  L  E  K  N  P  G  A  K  I  I  H  D  P  R  L  S  W  N  T
GTTCCTCGAAAAAAATCCCGGCGCGAAGATCATCCACGATCCACGTCTCTCCTGGAACAC  11400

 V  D  V  V  T  A  A  G  G  T  P  V  M  S  K  T  G  H  A  F
CGTTGATGTGGTGACTGCCGCAGGCGGCACCCCGGTAATGTCGAAAACCGGACACGCCTT  11460

 I  K  E  R  M  R  K  E  D  A  I  Y  G  G  E  M  S  A  H  H
TATTAAAGAACGTATGCGCAAGGAAGACGCCATCTACGGTGGCGAAATGAGCGCTCACCA  11520

 Y  F  R  D  F  A  Y  C  D  S  G  M  I  P  W  L  L  V  A  E
TTACTTCCGTGATTTCGCTTACTGCGACAGCGGCATGATCCCGTGGCTGCTGGTCGCCGA  11580

 L  V  C  L  K  G  K  T  L  G  E  M  V  R  D  R  M  A  A  F
ACTGGTGTGCCTGAAAGGAAAAACGCTGGGCGAAATGGTGCGCGACCGGATGGCGGCGTT  11640

 P  A  S  G  E  I  N  S  K  L  A  Q  P  V  E  A  I  N  R  V
TCCGGCAAGCGGTGAGATCAACAGCAAACTGGCGCAACCCGTTGAGGCAATTAATCGCGT  11700

 E  Q  H  F  S  R  E  A  L  A  V  D  R  T  D  G  I  S  M  T
GGAACAGCATTTTAGCCGCGAGGCGCTGGCGGTGGATCGCACCGATGGCATCAGCATGAC  11760

 F  A  D  W  R  F  N  L  R  S  S  N  T  E  P  V  V  R  L  N
CTTTGCCGACTGGCGCTTTAACCTGCGCTCCTCCAACACCGAACCGGTGGTGCGGTTGAA  11820

 V  E  S  R  G  D  V  K  L  M  E  K  K  T  K  A  L  L  K  L
TGTGGAATCACGCGGTGATGTAAAGCTAATGGAAAAGAAAACTAAAGCTCTTCTTAAATT  11880

     End of orf11
 L  S  E  *
GCTAAGTGAGTGATTATTTACATTAATCATTAAGCGTATTTAAGATTATATTAAAGTAAT  11940

GTTATTGCGGTATATGATGAATATGTGGGCTTTTTTATGTATAACGACTATACCGCAACT  12000

    Start of H-repeat
TTATCTAGGAAAAGATTAATAGAAATAAAGTTTTGTACTGACCAATTTGCATTTCACGTC  12060

ACGATTGAGACGTTCCTTTGCTTAAGACATTTTTTCATCGCTTATGTAATAACAAATGTG  12120

CCTTATATAAAAAGGAGAACAAAATGGAACTTAAAATAATTGAGACAATAGATTTTTATT  12180

ATCCCTGTTTACGATATTATAGCCAAAGTTGTATCCTGCATCAGTCCTGCAATATTTCAC  12240

GAGTGCTTTGTTAACTGAATACATGTCTGCCATTTTCCAGATGATAACGACGTCATCGCA  12300

ATTGATGGTAAAACACTTCGGCACACTTATGACAAGAGTCGTCGCAGAGGAGTGGTTCAT  12360
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GTCATTAGTGCGTTTCAGCAATGCACAGTCTGGTCCTCGGATAGATCAAGACGGATGAGA   12420
AACCTAATGCGTTCACAGTTATTCATGAACTTTCTAAAATGATGGGTATTAAAGGAAAAA   12480
TAATCATAACTGATGCGATGGCTTGCCAGAAAGATATTGCAGAGAAGATATAAAAACAGA   12540
GATGTGATTATTTATTCGCTGTAAAAGGAAATAAGAGTCGGCTTAATAGAGTCTTTGAGG   12600
AGATATTTACGCTGAAAGAATTAAATAATCCAAAACATGACAGTTACGCAATTAGTGAAA   12660
AGAGGCACGGCAGAGACGATGTCCGTCTTCATATTGTTTGAGATGCTCCTGATGAGCTTA   12720
TTGATTTCACGTTTGAATGGAAAGGGCTGCAGAATTTATGAATGGCAGTCCACTTTCTCT   12780
CAATAATAGCAGAGCAAAAGAAAGAATCCGAAATGACGATCAAATATTATATTAGATCTG   12840
CTGCTTTAACCGCAGAGAAGTTCGCCACAGTAAATCGAAATCACTGGCGCATGGAGAATA   12900
AGTTGCACAGTAGCCTGATGTGGTAATGAATGAAATCGACTATAATATAAGAAGGCGAGT   12960
TGCATTCGAATGATTTTCTAGAATGCGGCACATCGCTATTAATATCTGACAATGATAATG   13020
TATTCAAGGCAGGATTATCATGTAAGATGCGAAAAGCAGTCATGGACAGAAACTTCCTAG   13080

                                        End of the H-repeat
CGTCAGGCATTGCAGCGTGCGGGCTTTCATAATCTTGCAT TGGTTTGATAAGATATTTC   13140

                 Start of orf12
                 M  N  L  Y  G  I  F  G  A  G  S  Y  G  R  E
TTTGGAGATGGGAAAATGAATTTGTATGGTATTTTTGGTGCTGGAAGTTATGGTAGAGAA   13200

 T  I  P  I  L  N  Q  Q  I  K  Q  E  C  G  S  D  Y  A  L  V
ACAATACCCATTCTAAATCAACAAATAAAGCAAGAATGTGGTTCTGACTATGCTCTGGTT   13260

 F  V  D  D  V  L  A  G  K  K  V  N  G  F  E  V  L  S  T  N
TTTGTGGATGATGTTTTGGCAGGAAAGAAAGTTAATGGTTTTGAAGTGCTTTCAACCAAC   13320

 C  F  L  K  A  P  Y  L  K  K  Y  F  N  V  A  I  A  N  D  K
TGCTTTCTAAAAGCCCCTTATTTAAAAAAGTATTTTAATGTTGCTATTGCTAATGATAAG   13380

 I  R  Q  R  V  S  E  S  I  L  L  H  G  V  E  P  I  T  I  K
ATACGACAGAGAGTGTCTGAGTCAATATTATTACACGGGGTTGAACCAATAACTATAAAA   13440

 H  P  N  S  V  V  Y  D  H  T  M  I  G  S  G  A  I  I  S  P
CATCCAAATAGCGTTGTTTATGATCATACTATGATAGGTAGTGGCGCTATTATTTCTCCC   13500

 F  V  T  I  S  T  N  T  H  I  G  R  F  F  H  A  N  I  Y  S
TTTGTTACAATATCTACTAATACTCATATAGGGAGGTTTTTTCATGCAAACATATACTCA   13560

 Y  V  A  H  D  C  Q  I  G  D  Y  V  T  F  A  P  G  A  K  C
TACGTTGCACATGATTGTCAAATAGGAGACTATGTTACATTTGCTCCTGGGGCTAAATGT   13620

 N  G  Y  V  V  I  E  D  N  A  Y  I  G  S  G  A  V  I  K  Q
AATGGATATGTTGTTATTGAAGACAATGCATATATAGGCTCGGGTGCAGTAATTAAGCAG   13680

 G  V  P  N  R  P  L  I  I  G  A  G  A  I  I  G  M  G  A  V
GGTGTTCCTAATCGCCCACTTATTATTGGCGCGGGAGCCATTATAGGTATGGGGGCTGTT   13740

 V  T  K  S  V  P  A  G  I  T  V  C  G  N  P  A  R  E  M  K
GTCACTAAAAGTGTTCCTGCCGGTATAACTGTGTGCGGAAATCCAGCAAGAGAAATGAAA   13800

                   End of orf12
 R  S  P  T  S  I  *
AGATCGCCAACATCTATT TAATGGGAATGCGAAAACACGTTCCAAATGGGACTAATGTTT   13860
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AAAATATATATATAATTTCGCTAATTTACTAAATTATGGCTTCTTTTTAAGCTATCCTTTAC 13920

TTAGTTATTACTGATACAGCATGAAATTTATAATACTCTGATACATTTTTATACGTTATT 13980

CAAGCCGCATATCTAGCGGTAACCCCTGACAGGAGTAAACAATG 14024

Figure 6(1b)

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAATAATATCAACAAG
AACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGCGTATTAACAGC
GCGAAGGATGACGCCGCGGGTCAGGCGATTGCTAACCGTTTTACTTCTAACATTAAAGGC
CTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGTTGCACAGACCACTGAAGGC
GCGCTGTCCGAAATCAACAACAACTTACAGCGTATCCGTGAGCTGACGGTTCAGGCTTCT
ACCGGGACTAACTCTGATTCGGATCTGGACTCCATTCAGGACGAAATCAAATCCCGTCTC
GACGAAATTGACCGCGTATCCGGTCAGACCCAGTTCAACGGCGTGAACGTACTGGCAAAA
GACGGTTCGATGAAAATTCAGGTAGGTGCGAACGACGGCCAGACTATCACTATTGATCTG
AAGAAAATTGACTCTGATACGCTGGGGCTGAATGGTTTTAACGTGAATGGTTCCGGTACG
ATAGCCAATAAAGCGGCGACCATTAGCGACCTGACAGCAGCGAAAATGGATGCTGCAACT
AATACTATAACTACAACAAATAATGCGCTGACTGCATCAAAGGCCCTTGATCAACTGAAA
GATGGTGACACTGTTACTATCAAAGCAGATGCAGCTCAAACTGCCACGGTCTATACATAC
AATGCATCTGCTGGTAACTTCTCATTCAGTAATGTATCGAATAATACTTCAGCAAAAGCA
GGTGATGTAGCAGCTAGCCTTCTCCCGCCGGCTGGGCAAACTGCTAGTGGTGTTTACAAA
GCAGCAAGCGGTGAAGTGAACTTTGATGTTGATGCGAATGGTAAAATTACAATCGGAGGA
CAGGAAGCCTATTTAACTAGTGATGGTAACTTAACTACAAACGATGCTGGTGGTGCGACT
GCGGCTACGCTTGATGGTTTATTCAAGAAAGCTGGTGATGGTCAATCAATCGGGTTTAAT
AAGACTGCATCAGTCACGATGGGGGGAACAACTTATAACTTTAAAACGGGTGCTGATGCT
GGTGCTGCAACTGCTAACGCAGGGGTATCGTTCACTGATACAGCTAGCAAAGAAACCGTT
TTAAATAAAGTGGCTACAGCTAAACAAGGCACAGCAGTTGCAGCTAACGGTGATACATCC
GCAACAATTACCTATAAATCTGGCGTTCAGACGTATCAGGCGGTATTTGCCGCAGGTGAC
GGTACTGCTAGCGCAAAATATGCCGATAATACTGACGTTTCTAATGCAACAGCAACATAC
ACAGATGCTGATGGTGAAATGACTACAATTGGTTCATACACCACGAAGTATTCAATCGAT
GCTAACAACGGCAAGGTAACTGTTGATTCTGGAACTGGTTCGGGTAAATATGCGCCGAAA
GTCGGGGCTGAAGTATATGTTAGTGCTAATGGTACTTTAACAACAGATGCAACTAGCGAA
GGCACAGTAACAAAAGATCCACTGAAAGCTCTGGATGAAGCTATCAGCTCCATCGACAAA
TTCCGTTCATCCCTGGGGGCTATCCAAAACCGTTTGGATTCCGCCGTCACCAACCTGAAC
AACACCACTACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACC
GAAGTGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCCGGTAACTCCGTGCTGGCA
AAAGCCAACCAGGTACCGCAGCAGGTTCTGTCTCTACTGCAGGGTTAA

Figure 7

AACAAATCTCAGTCTTCTCTTAGCTCTGCTATT
GAGCGTCTGTCTTCTGGTCTGCGTATTAACAGCGCAAAAGACGATGCAGCAGGTCAGGCG
ATTGCTAACCGTTTTACGGCAAATATTAAAGGTCTGACCCAGGCTTCCCGTAACGCAAAT
GATGGTATTTCTGTTGCGCAGACCACTGAAGGTGCGCTGAATGAAATTAACAACAACCTG
CAGCGTATTCGTGAACTTTCTGTTCAGGCAACTAACGGTACTAACTCTGACAGTGACCTG
ACCTCCATCCAGTCCGAAATCCAGCAGCGTCTGAGTGAAATTGACCGTGTTTCTGGTCAG
ACTCAGTTTAACGGCGTTAAAGTGCTGGCTTCTGATCAGGATATGACTATTCAGGTTGGT
GCAAACGACGGCGAAACAATTACTATTAAACTGCAGGAAATTAATTCCGACACACTGGGA
TTATCTGGTTTTGGTATTAAAGATCCTACTAAATTAAAAGCCGCAACGGCTGAAACAACC
TATTTTGGATCGACAGTTAAGCTTGCTGACGCTAATACACTTGATGCAGATATTACAGCT
ACAGTTAAAGGCACTACGACTCCGGGCCAACGTGACGGTAATATTATGTCTGATGCTAAC
GGTAAGTTGTACGTTAAAGTTGCCGGTTCAGATAAACCCGCTGAAAATGGTTATTATGAA
GTTACTGTGGAGGATGATCCGACATCTCCTGATGCAGGTAAGCTGAAGCTGGGGGCTCTA
GCGGGTACCCAGCCTCAAGCTGGTAATTTAAAGGAAGTCACAACGGTGAAAGGGAAGGGG
GCTATTGATGTTCAGTTGGGTACTGATACCGCAACCGCTTCTATCACAGGTGCAAAACTC
TTTAAGTTAGAAGACGCCAATGGCAAAGATACTGGTTCATTTGCGTTGATTGGTGATGAC
GGTAAACAGTATGCAGCGAATGTTGATCAGAAAACAGGAGCAGTTTCCGTTAAAACAATG
TCTTACACTGATGCTGACGGTGTCAAACACGACAATGTTAAAGTTGAACTGGGTGGAAGC
GATGGCAAAACCGAAGTTGTAACTGCAACCGATGGCAAAACTTACAGTGTTAGTGATTTA
CAAGGTAAGAGCCTGAAAACTGATTCTATTGCAGCAATTTCTACGCAGAAAACAGAAGAT
CCTTTGGCTGCTATCGATAAAGCACTGTCTCAGGTTGACTCGTTGCGTTCTAACCTAGGT
GCAATTCAAAATCGTTTCGACTCTGCCATCACCAACCTTGGCAACACCGTAAACAACCTG
TCTTCTGCCCGTAGCCGTATCGAAGATGCTGACTACGCGACCGAAGTGTCTAACATGTCT
CGTGCGCAGATCCTGCAACAAGCGGGTACCTCTGTTCTGGCGCAG

Figure 8

AACAAATCTCAGTCTTCTCTGAGCTTCGCCATTGAACGTCTCTCTTC
TGGCCTGCGTATTAACAGTGCTAAAGATGACGCAGCAGGTCAGGCGATTGCTAACCGTTT
TACAGCAAATATTAAAGGTCTGACTCAGGCTTCCCGTAACGCGAATGATGGTATTTCTGT
TGCGCAGACCACTGAAGGTGCGCTTTCTGAAATCAACAATAACTTACAGCGTATTCGTGA
ATTGTCAGTACAGGCCACTAATGGTACAAACTCTGACTCCGACCTGAATTCAATTCAGGA
TGAAATTACACAACGCCTTAGTGAAATTGATCGTGTTTCTAACCAGACACAATTTAATGG
TGTAAAAGTTCTGGCTTCTGATCAGACTATGAAAATTCAAGTAGGTGCGAACGATGGTGA
AACCATTGAGATTGCCCTTGATAAAATTGATGCTAAAACCTTGGGGCTTGATAACTTTAG
CGTAGCACCAGGAAAAGTTCCAATGTCCTCTGCGGTTGCACTTAAGAGCGAAGCCGCTCC
TGACTTAACTAAGGTAAATGCAACTGATGGTAGTGTGGGAGGTGCTAAAGCATTCGGTAG
CAATTATAAAAATGCTGATGTTGAAACTTATTTTGGTACCGGTAATGTACAAGATACAAA
GGATACAACTGATGCGACCGGTACTGCAGGAACAAAAGTTTATCAAGTACAGGTGGAAGG
GCAGACTTATTTTGTTGGTCAAGATAATAATACCAACACGAACGGTTTTACATTATTGAA
ACAAAACTCTACAGGTTATGAAAAAGTTCAGGTGGGTGGTAAGGATGTTCAGTTAGCAAA
CTTTGGTGGTCGTGTAACTGCATTTGTTGAAGATAATGGTTCTGCCACATCAGTTGATTT
AGCTGCGGGTAAAATGGGTAAAGCATTAGCTTATAATGATGCACCAATGTCTGTTTATTT
TGGGGGAAAAAACCTAGATGTCCACCAAGTACAAGATACCCAAGGGAATCCTGTACCTAA
TTCATTTGCTGCTAAAACATCAGACGGCACCTACATTGCAGTAAATGTAGATGCCGCTAC
AGGTAACACGTCTGTTATTACTGATCCTAATGGTAAGGCAGTTGAATGGGCAGTAAAAAA
TGATGGTTCTGCACAGGCAATTATGCGTGAAGATGATAAGGTTTATACAGCCAATATCAC
GAATAAGACGGCAACCAAAGGTGCTGAACTCAGTGCCTCAGATTTGAAAGCCTTAGCAAC
CACAAATCCATTATCCACATTAGACGAAGCTTTGGCAAAAGTTGATAAGTTGCGCAGTTC
TTTGGGTGCAGTACAAAACCGTTTCGACTCTGCCATCACCAACCTTGGCAACACCGTAAA
CAACCTGTCTTCTGCCCGTAGCCGTATAGAAGATGCTGACTACGCAACCGAAGTGTCTAA
CATGTCTCGTGCGCAGATCCTGCAACAAGCGGGTACCTCTGTTCTGGCACAG

Figure 9

AACAAAAACCAGTCTGCGCTGTCGACTTCTATCGAG
CGCCTCTCTTCTGGTCTGCGTATTAACAGCGCTAAAGATGACGCCGCGGGCCAGGCGATT
GCTAACCGCTTTACTTCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAACGAC
GGTATTTCTCTGGCGCAGACGGCTGAAGGCGCGCTGTCAGAGATTAACAACAACTTGCAG
CGTATTCGTGAACTGACCGTTCAGGCCTCTACCGGCACGAACTCTGATTCCGACCTGTCT
TCTATTCAGGACGAAATCAAATCCCGTCTTGATGAAATTGACCGTGTATCTGGTCAGACC
CAGTTCAACGGTGTGAACGTGCTGTCGAAAAACGATTCGATGAAGATTCAGATTGGTGCC
AATGATAACCAGACGATCAGCATTGGCTTGCAACAAATCGACAGTACCACTTTGAATCTG
AAAGGATTTACCGTGTCCGGCATGGCGGATTTCAGCGCGGCGAAACTGACGGCTGCTGAT
GGTACAGCAATTGCTGCTGCGGATGTCAAGGATGCTGGGGGTAAACAAGTCAATTTACTG
TCTTACACTGACACCGCGTCTAACAGTACTAAATATGCGGTCGTTGATTCTGCAACCGGT
AAATACATGGAAGCCACTGTAGTCATTACCGGTACGGCGGCGGCGGTAACTGTTGGTGCA
GCGGAAGTGGCGGGAGCCGCTACAGCCGATCCGTTAAAAGCACTGGATGCCGCAATCGCT
AAAGTCGACAAATTCCGCTCCTCCCTCGGTGCCGTTCAAAACCGTCTGGATTCTGCGGTC
ACCAACCTGAACAACACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCC
GACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCGGGCAAC TCCGTGCTGTCTAA

Figure 10

AACAAAAACCAGTCTGCGCTGTCGACTTCTAT
CGAGCGCCTCTCTTCTGGTCTGCGTATTAACAGCGCTAAAGATGACGCCGCGGGCCAGGC
GATTGCTAACCGCTTCACTTCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAA
CGACGGTATCTCTCTGGCGCAGACCACTGAAGGCGCGCTGTCTGAAATCAACAACAACTT
GCAGCGTGTGCGTGAGTTGACCGTTCAGGCGACGACCGGGACTAACTCTGATTCTGACCT
GTCTTCTATTCAGGACGAAATCAAATCCCGTCTGGATGAAATTGATCGCGTTTCCGGTCA
GACCCAGTTCAACGGCGTGAATGTGCTGGCGAAAGATGGTTCGATGAAGATTCAGGTTGG
CGCGAATGATGGGCAGACTATTAGCATTGATTTGCAGAAGATTGACTCTTCTACATTAGG
ACTGAACGGTTTCTCCGTTTCGGGTCAGTCACTTAACGTTAGTGATTCCATTACTCAAAT
TACCGGTGCCGCCGGGACAAAACCTGTTGGTGTTGATTTCACTGCTGTTGCGAAAGATCT
GACTACTGCGACAGGTAAAACAGTCGATGTTTCTAGCCTGACGTTACACAACACTCTGGA
TGCGAAAGGGGCTGCTACATCACAGTTCGTCGTTCAATCCGGCAATGATTTCTACTCCGC
GTCGATTAATCATACAGACGGCAAAGTCACGTTGAATAAAGCCGATGTCGAATACACAGA
CACCGATAATGGACTAACGACTGCGGCTACTCAGAAAGATCAACTGATTAAAGTTGCCGC
TGACTCTGACGGCTCGGCTGCGGGATATGTAACATTCCAAGGTAAAAACTACGCTACAAC
GGTTTCAACGGCACTTGATGATAATACTGCGGCAAAAGCAACAGATAATAAAGTTGTTGT
TGAATTATCAACAGCAAAACCGACTGCACAGTTCTCAGGGGCTTCTTCTGCTGATCCACT
GGCACTTTTAGACAAAGCTATTGCACAGGTTGATACTTTCCGCTCCTCCCTCGGTGCGGT
GCAAAACCGTCTGGATTCCGCAGTAACCAACCTGAACAACACCACCACCAACCTGTCTGA
AGCGCAGTCCCGTATTCAGGACGCCGACTATGCTACAGAAGTGTCCAACATGTCGAAAGC
GCAGATCATCCAGCAGGCAGGTAACTCGGTGCTGTCCAAA

Figure 11

ATGGCACAAGTCATTAATACCAACAGCCTCTCGC
TGATCACTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTC
TGTCTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCGGGTCAGGCGATTGCTA
ACCGTTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTA
TTTCTGTTGCGCAGACCACCGAAGGCGCGCTGTCCGAAATTAACAACAACTTACAGCGTA
TTCGTGAACTGACGGTTCAGGCTTCTACCGGGACTAACTCTGATTCGGATCTGGACTCCA
TTCAGGACGAAATCAAATCCCGTCTCGACGAAATTGACCGCGTATCCGGTCAGACCCAGT
TCAACGGCGTGAACGTACTGGCAAAAGACGGTTCGATGAAAATTCAGGTTGGTGCGAATG
ACGGCCAGACTATCACTATTGATCTGAAGAAAATTGACTCTGATACGCTGGGGCTGAATG
GGTTTAATGTGAACGGCAAAGGGGAAACGGCTAATACGGCAGCAACCCTGAAAGATATGT
CTGGATTCACAGCTGCGGCGGCACCAGGGGGAACTGTTGGTGTAACTCAATATACTGACA
AATCGGCTGTAGCAAGTAGCGTAGATATTCTAAATGCTGTTGCTGGCGCAGATGGAAATA
AAGTTACAACTAGCGCCGATGTTGGTTTTGGTACACCAGCCGCTGCTGTAACCTATACCT
ACAATAAAGACACTAATTCATATTCCGCCGCTTCTGATGATATTTCCAGCGCTAACCTGG
CTGCTTTCCTCAATCCTCAGGCCGGAGATACGACTAAAGCTACAGTTACAATTGGTGGCA
AAGATCAAGATGTAAACATCGATAAATCCGGTAATTTAACTGCTGCTGATGATGGCGCAG
TACTTTATATGGATGCTACCGGTAACTTAACTAAAAATAATGCTGGTGGTGATACACAAG
CTACTTTGGCTAAACTTGCTACTGCTACTGGTGCTAAAGCCGCGACCATCCAAACTGATA
AAGGAACATTCACCAGTGACGGTACAGCGTTTGATGGTGCATCAATGTCCATTGATACCA
ATACATTTGCAAATGCAGTAAAAAATGACACTTATACTGCCACTGTAGGTGCTAAGACTT
ATAGCGTAACAACAGGTTCTGCTGCTGCAGACACCGCTTATATGAGCAATGGGGTTCTCA
GTGATACTCCGCCAACTTACTATGCACAAGCTGATGGAAGTATCACAACTACTGAGGATG
CGGCTGCCGGTAAACTGGTCTACAAAGGTTCCGATGGTAAGTTAACAACGGATACGACTA
GCAAAGCAGAATCAACATCAGATCCGCTGGCAGCTCTTGACGACGCTATCAGCCAGATCG
ACAAATTCCGCTCCTCCCTGGGTGCGGTGCAAAACCGTCTGGATTCCGCAGTGACCAACC
TGAACAACACCACTACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATG
CGACCGAAGTGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCCGGTAACTCCGTGC
TGGCAAAAGCTAACCAGGTTCCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 12

ATGGCACAAG TCATTAATAC CAACAGCCTC TCGCTGATCA CTCAAAATAA TATCAACAAG
AACCAGTCTG CGCTGTCGAG TTCTATCGAG CGTCTGTCTT CTGGCTTGCG TATTAACAGC
GCGAAGGATG ACGCCGCGGG TCAGGCGATT GCTAACCGTT TTACTTCTAA CATTAAAGGC
CTGACTCAGG CTGCACGTAA CGCCAACGAC GGTATTTCTG TTGCACAGAC CACCGAAGGC
GCGCTGTCTG AAATCAACAA CAACTTACAG CGTATCCGTG AGCTGACGGT TCAGGCTTCT
ACCGGAACTA ACTCTGATTC GGATCTGGAC TCCATTCAGG ACGAAATCAA ATCCCGTCTT
GATGAAATTG ACCGCGTATC CGGCCAGACC CAGTTCAACG GCGTGAACGT ACTGGCAAAA
GACGGTTCGA TGAAAATTCA GGTTGGTGCG AATGACGGTG AAACTATCAC TATCGACCTG
AAGAAAATCG ATTCTGATAC TCTGGGTCTG AATGGTTTTA ACGTAAATGG TAAAGGTACT
ATTACCAACA AAGCTGCAAC GGTAAGTGAT TTAACTTCTG CTGGCGCGAA GTTAAACAC
CACGACAGGT CTTTATGATC TGAAAACCGA AAATACCTTG TTAACTACCG ATGCTGCATT
CGATAAATTA GGGAATGGCG ATAAAGTCAC CGTTGGCGGC GTAGATTATA CTTACAACGC
TAAATCTGGT GATTTTACTA CCACCAAATC TACTGCTGGT ACGGGTGTAG ACGCCGCGGC
GCAGGCTACT GATTCAGCTA AAAAACGTGA TGCGTTAGCT GCCACCCTTC ATGCTGATGT
GGGTAAATCT GTTAATGGTT CTTACACCAC AAAAGATGGT ACTGTTTCTT TCGAAACGGA
TTCAGCAGGT AATATCACCA TCGGTGGAAG CCAGGCATAC GTAGACGATG CAGGCAACTT
GACGACTAAC AACGCTGGTA GCGCAGCTAA AGCTGATATG AAAGCGCTGC TTAAAGCCGC
GAGCGAAGGT AGTGACGGTG CTTCTCTGAC ATTCAATGGC ACTGAATATA CTATCGCAAA
AGCAACTCCT GCGACAACCT CTCCAGTAGC TCCGTTAATC CCTGGTGGGA TTACTTATCA
GGCTACAGTG AGTAAAGATG TAGTATTGAG CGAAACCAAA GCGGCTGCCG CGACATCTTC
AATTACCTTT AATTCCGGTG TACTGAGCAA AACTATTGGG TTTACCGCGG GTGAATCCAG
TGATGCTGCG AAGTCTTATG TGGATGATAA AGGTGGTATT ACTAACGTTG CCGACTATAC
AGTCTCTTAC AGCGTTAACA AGGATAACGG CTCTGTGACT GTTGCCGGGT ATGCTTCAGC
GACTGATACC AATAAAGATT ATGCTCCAGC AATTGGTACT GCTGTAAATG TGAACTCCGC
GGGTAAAATC ACTACTGAGA CTACCAGTGC TGGTTCTGCA ACGACCAACC CGCTTGCTGC
CCTGGACGAC GCTATCAGCT CCATCGACAA ATTCCGTTCT TCCCTGGGTG CTATCCAGAA
CCGTCTGGAT TCCGCAGTCA CCAACCTGAA CAACACCACT ACCAACCTGT CTGAAGCGCA
GTCCCGTATT CAGGACGCCG ACTATGCGAC CGAAGTGTCC AACATGTCGA AAGCGCAGAT
TATCCAGCAG GCCGGTAACT CCGTGCTGGC AAAAGCCAAC CAGGTACCGC AGCAGGTTCT
GTCTCTGCTG CAGGGTTAA

Figure 13

AACAAATCTCAGTCTTCTCTTAGCTCTGCTA
TTGAGCGTCTGTCTTCTGGTCTGCGTATTAACAGCGCAAAAGACGATGCAGCAGGTCAGG
CGATTGCTAACCGTTTTACGGCAAATATTAAAGGTCTGACCCAGGCTTCCCGTAACGCAA
ATGATGGTATTTCTGTTGCGCAGACCACTGAAGGTGCGCTGAATGAAATTAACAACAACC
TGCAGCGTATTCGTGAACTTTCTGTTCAGGCAACTAACGGTACTAACTCTGACAGCGATC
TTTCTTCTATCCAGGCTGAAATTACTCAACGTCTGGAAGAAATTGACCGTGTATCTGAGC
AAACTCAGTTTAACGGCGTGAAAGTCCTTGCTGAAAATAATGAAATGAAAATTCAGGTTG
GTGCTAATGATGGTGAAACCATCACTATCAATCTGGCAAAAATTGATGCGAAAACTCTCG
GCCTGGACGGTTTTAATATCGATGGCGCGCAGAAAGCAACAGGCAGTGACCTGATTTCTA
AATTTAAAGCGACAGGTACTGATAATTATGATGTTGGCGGTAAAACTTATACCGTGAATG
TGGAGAGCGGCGCGGTTAAGAATGATGCTAATAAAGATGTTTTTGTAAGCGCAGCTGATG
GATCGCTGACGACCAGTAGTGATACTAAAGTATCCGGTGAAAGTATTGATGCAACAGAAC
TAGCGAAACTTGCAATAAAATTAGCTGACAAAGGCTCCATTGAATACAAGGGCATTACAT
TTACTAACAACACTGGCGCAGAGCTTGATGCTAATGGTAAAGGTGTTTTGACCGCAAATA
TTGATGGTCAAGATGTTCAATTTACTATTGACAGTAATGCACCCACGGGTGCCGGCGCAA
CAATAACTACAGACACAGCTGTTTACAAAAACAGTGCGGGCCAGTTCACCACTACAAAAG
TGGAAAATAAAGCCGCAACACTCTCTGATCTGGATCTTAATGCAGCCAAGAAAACAGGTA
GCACTTTAGTTGTAAATGGCGCCACCTACAATGTCAGCGCAGATGGTAAAACGGTAACTG
ATACTACTCCTGGTGCCCCTAAAGTGATGTATCTGAGCAAATCAGAAGGTGGTAGCCCGA
TTCTGGTAAACGAAGATGCAGCAAAATCGTTGCAATCTACCACCAACCCGCTCGAAACTA
TCGACAAGGCATTGGCTAAAGTTGACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACC
GTTTCGACTCTGCCATCACCAACCTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTA
GCCGTATCGAAGATGCTGACTACGCGACCGAAGTGTCTAACATGTCTCGTGCGCAGATCC
TGCAACAAGCGGGTACCTCTGTTCTGGCGCAG

Figure 14

ATGGCACAAGTCATTAATACCAACAGCCTCTCG
CTGATCACTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGT
CTGTCTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCGGGTCAGGCGATTGCT
AACCGTTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGT
ATTTCCGTTGCACAGACCACTGAAGGCGCGCTGTCCGAAATTAACAACAACTTACAGCGT
ATTCGTGAACTGACGGTTCAGGCTTCTACCGGGACTAACTCCGATTCGGATCTGGACTCC
ATTCAGGACGAAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCCGGCCAGACCCAG
TTCAACGGCGTGAACGTGCTGTCCAAAGATGGCTCGATGAAAATTCAGGTCGGCGCGAAC
GATGGCGAAACGATTACTATTGATCTGAAGAAAATTGACTCTGATACGCTGAATCTGGCT
GGTTTTAACGTTAACGGTAAAGGTTCTGTAGCGAATACAGCTGCGACAAGCGACGATTTA
AAACTGGCTGGTTTCACTAAGGGCACCACAGATACCAATGGCGTGACCGCGTATACAAAC
ACAATTAGTAATGACAAAGCCAAAGCTTCCGATCTGTTAGCTAATATCACCGATGGATCA
GTGATCACTGGGGGAGGGGCAAACGCTTTTGGCGTGGCTGCAAAGAATGGTTACACCTAT
GATGCAGCAAGTAAATCTTATAGTTTTGCTGCAGATGGTGCCGATTCAGCGAAGACGTTA
AGCATCATTAATCCAAACACCGGTGATTCGTCGCAGGCGACAGTGACTATTGGTGGTAAA
GAGCAGAAAGTTAATATTTCCCAGGATGGAAAAATTACTGCGGCAGATGATAATGCGACG
CTGTATTTAGATAAACAGGGAAACTTGACAAAAACGAATGCAGGTAACGATACCGCAGCG
ACTTGGGATGGTTTAATTTCCAACAGCGATTCTACCGGTGCGGTTCCAGTTGGGGTTGCA
ACTACAATTACAATTACTTCTGGTACAGCTTCCGGAATGTCTGTTCAGTCCGCAGGAGCA
GGAATTCAGACCTCAACAAATTCTCAGATTCTTGCAGGTGGTGCATTTGCGGCTAAGGTA
AGTATTGAGGGAGGCGCTGCTACAGACATTTTGGTAGCAAGTAATGGAAACATAACAGCG
GCTGATGGTAGTGCACTTTATCTTGATGCGACTACTGGTGGATTCACTACAACGGCTGGA
GGAAATACAGCTGCTTCGTTAGATAATTTAATTGCTAACAGTAAGGATGCTACCTTAACC
GTAACTTCAGGTACCGGCCAGAACACTGTTTATAGCACAACAGGAAGTGGCGCTCAGTTC
ACCAGTTTAGCAAAAGTAGACACAGTCAATGTCACCAACGCACATGTCAGTGCCGAAGGT
ATGGCAAATCTGACAAAAAGCAATTTTACCATTGATATGGGCGGTACAGGTACAGTAACT
TACACAGTTTCCAATGGGGATGTGAAAGCTGCTGCAAATGCTGATGTTTATGTCGAAGAT
GGTGCACTTTCAGCCAATGCTACAAAAGATGTAACCTACTTTGAACAAAAAAATGGGGCT
ATTACCAACAGCACCGGTGGTACCATCTATGAAACAGCTGATGGTAAGTTAACAACAGAA
GCTACTACTGCATCCAGTTCCACCGCCGATCCCCTGAAAGCTCTGGACGAAGCCATCAGC
TCCATCGACAAATTCCGCTCCTCCCTCGGTGCGGTGCAAAACCGTCTGGATTCCGCGGTC
ACCAACCTGAACAACACCACTACCAACCTGTCCGAAGCGCAGTCCCGTATTCAGGACGCC
GACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATCATCCAGCAGGCCGGTAAC
TCCGTGCTGGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 15

ATGGCACAAGTCATTAATACCAACAGC
CTCTCGCTGATCACTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATC
GAGCGTCTGTCTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCGGGTCAGGCG
ATTGCTAACCGTTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAAC
GACGGTATTTCTGTTGCGCAGACCACCGAAGGCGCGCTGTCCGAAATTAACAACAACTTA
CAGCGTGTGCGTGAGCTGACTGTTCAGGCGACCACCGGTACTAACTCTGAGTCTGACCTG
TCTTCTATCCAGGACGAAATCAAATCTCGCCTGGAAGAGATTGATCGTGTTTCAAGTCAG
ACTCAATTTAACGGCGTGAATGTTTTGGCTAAAGATGGGAAAATGAACATTCAGGTTGGG
GCAAATGATGGACAGACTATCACTATTGATCTGAAAAAGATCGATTCATCTACACTAAAC
CTCTCCAGTTTTGATGCTACAAACTTGGGCACCAGTGTTAAAGATGGGGCCACCATCAAT
AAGCAAGTGGCAGTAGGTGCTGGCGACTTTAAAGATAAAGCTTCAGGATCGTTAGGTACC
CTAAAATTAGTTGAGAAAGACGGTAAGTACTATGTAAATGACACTAAAAGTAGTAAGTAC
TACGATGCCGAAGTAGATACTAGTAAGGGTAAAATTAACTTCAACTCTACAAATGAAAGT
GGAACTACTCCTACTGCAGCGACGGAAGTAACTACTGTTGGCCGCGATGTAAAATTGGAT
GCTTCTGCACTTAAAGCCAACCAATCGCTTGTCGTGTATAAAGATAAAAGCGGCAATGAT
GCTTATATCATTCAGACCAAAGATGTAACAACTAATCAATCAACTTTCAATGCCGCTAAT
ATCAGTGATGCTGGTGTTTTATCTATTGGTGCATCTACAACCGCGCCAAGCAATTTAACA
GCTAACCCGCTTAAGGCTCTTGATGATGCAATTGCATCTGTTGATAAATTCCGCTCTTCT
CTCGGTGCCGTTCAGAACCGTCTGGATTCTGCCATTGCCAACCTGAACAACACCACTACC
AACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCTGACTATGCGACCGAAGTGTCCAAC
ATGTCGAAAGCGCAGATTATCCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCCAACCAG
GTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 16

AACAAATCTCAGTCTTCTCTGAGCTCCGCCAT
TGAACGTCTCTCTTCTGGCCTGCGTATTAACAGTGCTAAAGATGACGCAGCAGGTCAGGC
GATTGCTAACCGTTTTACAGCAAATATTAAAGGTCTGACTCAGGCTTCCCGTAACGCGAA
TGATGGTATTTCTGTTGCGCAGACCACTGAAGGTGCGCTGAATGAAATTAACAACAACCT
GCAGCGTGTACGTGAACTGACTGTTCAGGCAACTAACGGTACTAACTCTGACAGCGATCT
TTCTTCTATCCAGGCTGAAATTACTCAACGTCTGGAAGAAATTGACCGTGTATCTGAGCA
AACTCAGTTTAACGGCGTGAAAGTCCTTGCTGAAAATAATGAAATGAAAATTCAGGTTGG
TGCTAATGATGGTGAAACCATCACTATCAATCTGGCAAAAATTGATGCGAAAACTCTCGG
CCTGGACGGTTTTAATATCGATGGCGCGCAGAAAGCAACTGGCAGTGACCTGATTTCTAA
ATTTAAAGCGACAGGTACTGATAACTATGATGTTGGCGGTGATGCTTATACTGTTAACGT
AGATAGCGGAGCTGTTAAAGATACTACAGGGAATGATATTTTTGTTAGTGCAGCAGATGG
TTCACTGACAACTAAATCTGACACAAACATAGCTGGTACAGGGATTGATGCTACAGCACT
CGCAGCAGCGGCTAAGAATAAAGCACAGAATGATAAATTCACGTTTAATGGAGTTGAATT
CACAACAACAACTGCAGCGGATGGCAATGGGAATGGTGTATATTCTGCAGAAATTGATGG
TAAGTCAGTGACATTTACTGTGACAGATGCTGACAAAAAAGCTTCTTTGATTACGAGTGA
GACAGTTTACAAAAATAGCGCTGGCCTTTATACGACAACCAAAGTTGATAACAAGGCTGC
CACACTTTCCGATCTTGATCTCAATGCAGCTAAGAAAACAGGAAGCACGTTAGTTGTTAA
CGGTGCAACTTACGATGTTAGTGCAGATGGTAAAACGATAACGGAGACTGCTTCTGGTAA
CAATAAAGTCATGTATCTGAGCAAATCAGAAGGTGGTAGCCCGATTCTGGTAAACGAAGA
TGCAGCAAAATCGTTGCAATCTACCACCAACCCGCTCGAAACTATCGACAAAGCATTGGC
TAAAGTTGACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACCGTTTCGACTCTGCTAT
CACCAACCTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTAGCCGTATCGAAGATGC
TGACTACGCGACCGAAGTGTCTAACATGTCTCGTGCGCAGATCCTGCAACAAGCGGGTAC
CTCTGTTCTGGCGCAG

Figure 17

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCA
CTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTT
CTGGCTTGCGTATTAACAGCGCGAAGGATGACGCAGCGGGTCAGGCGATTGCTAACCGTT
TCACCTCTAACATTAAAGGCCTGACTCAGGCGGCCCGTAACGCCAACGACGGTATCTCCG
TTGCGCAGACCACCGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATCCGTG
AACTGACGGTTCAGGCTTCTACCGGGACTAACTCCGATTCGGATCTGGACTCCATTCAGG
ACGAAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCTGGCCAGACCCAGTTCAACG
GCGTGAACGTACTGGCGAAAGACGGTTCAATGAAAATTCAGGTTGGTGCGAATGACGGCC
AGACTATCACGATTGATCTGAAGAAAATTGACTCAGATACGCTGGGGCTGAATGGTTTTA
ACGTGAATGGTTCCGGTACGATAGCCAATAAAGCGGCGACCATTAGCGACCTGACAGCAG
CGAAAATGGATGCTGCAACTAATACTATAACTACAACAAATAATGCGCTGACTGCATCAA
AGGCGCTTGATCAACTGAAAGATGGTGACACTGTTACTATCAAAGCAGATGCTGCTCAAA
CTGCCACGGTTTATACATACAATGCATCAGCTGGTAACTTCTCATTCAGTAATGTATCGA
ATAATACTTCAGCAAAAGCAGGTGATGTAGCAGCTAGCCTTCTCCCGCCGGCTGGCAAA
CTGCTAGTGGTGTTTATAAAGCAGCAAGCGGTGAAGTGAACTTTGATGTTGATGCGAATG
GTAAAATCACAATCGGAGGACAGAAAGCATATTTAACTAGTGATGGTAACTTAACTACAA
ACGATGCTGGTGGTGCGACTGCGGCTACGCTTGATGGTTTATTCAAGAAAGCTGGTGATG
GTCAATCAATCGGGTTTAAGAAGACTGCATCAGTCACGATGGGGGAACAACTTATAACT
TTAAAACGGGTGCTGATGCTGATGCTGCAACTGCTAACGCAGGGGTATCGTTCACTGATA
CAGCTAGCAAAGAAACCGTTTTAAATAAAGTGGCTACAGCTAAACAAGGCAAAGCAGTTG
CAGCTGACGGTGATACATCCGCAACAATTACCTATAAATCTGGCGTTCAGACGTATCAGG
CTGTATTTGCCGCAGGTGACGGTACTGCTAGCGCAAAATATGCCGATAAAGCTGACGTTT
CTAATGCAACAGCAACATACACTGATGCTGATGGTGAAATGACTACAATTGGTTCATACA
CCACGAAGTATTCAATCGATGCTAACAACGGCAAGGTAACTGTTGATTCTGGAACTGGTA
CGGGTAAATATGCGCCGAAAGTAGGGGCTGAAGTATATGTTAGTGCTAATGGTACTTTAA
CAACAGATGCAACTAGCGAAGGCACAGTAACAAAAGATCCACTGAAAGCTCTGGATGAAG
CTATCAGCTCCATCGACAAATTCCGTTCTTCCCTGGGTGCTATCCAGAACCGTCTGGATT
CCGCAGTCACCAACCTGAACAACACCACTACCAACCTGTCCGAAGCGCAGTCCCGTATTC
AGGACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATCATTCAGCAGG
CCGGTAACTCCGTGCTGGCAAAAGCCAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGC AGGGTTAA

Figure 18

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCAGTCAAAATA
ATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGC
GTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTTACTTCTA
ACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCCGTTGCGCAGA
CCACTGAAGGTGCGCTGTCCGAAATCAACAACAACTTACAGCGTATTCGTGAGCTGACGG
TTCAGGCTTCTACCGGGACTAACTCCGATTCTGACCTGGACTCCATCCAGGACGAAATCA
AGTCTCGTCTGGACGAAATTGACCGCGTATCCGGTCAGACCCAGTTCAACGGCGTGAACG
TGCTGGCGAAAGACGGTTCGATGAAAATTCAGGTTGGTGCGAATGACGGCCAGACTATCA
CGATTGATCTGAAGAAAATTGACTCAGATACGCTGGGGCTGAGTGGGTTTAATGTGAATG
GTGGCGGGGCTGTTGCTAACACTGCTGCATCTAAAGCTGACTTGGTAGCTGCTAATGCAA
CTGTGGTAGGCAACAAATATACTGTGAGTGCGGGTTACGATGCTGCTAAAGCGTCTGATT
TGCTGGCTGGAGTTAGTGATGGTGATACTGTTCAGGCAACCATTAATAACGGCTTCGGAA
CGGCGGCTAGTGCAACGAATTACAAGTATGACAGTGCAAGTAAGTCTTACTCTTTTGATA
CCACAACGGCTTCAGCTGCCGATGTTCAGAAATATTTGACCCCGGGCGTTGGTGATACCG
CTAAGGGCACTATTACTATCGATGGTTCTGCACAGGATGTTCAGATCAGCAGTGATGGTA
AAATTACGTCAAGCAATGGAGATAAACTTTACATTGATACAACTGGGCGCTTAACGAAAA
ACGGCTTTAGTGCTTCTTTGACTGAGGCTAGTCTGTCCACACTTGCAGCCAATAATACCA
AAGCGACAACCATTGACATTGGCGGTACCTCTATCTCCTTTACCGGTAATAGTACTACGC
CGAACACTATTACTTATTCAGTAACAGGTGCAAAAGTTGATCAGGCAGCTTTCGATAAAG
CTGTATCAACCTCTGGAAACGATGTTGATTTCACTACCGCAGGTTATAGCGTCGACGGCG
CAACTGGCGCTGTAACAAAAGGTGTTGCTCCGGTTTATATTGATAACAACGGGGCGTTGA
CCACATCTGATACTGTAGATTTTTATCTACAGGATGATGGTTCAGTGACTAACGGCAGCG
GTAAGGCAGTTTATAAAGATGCTGACGGTAAATTGACGACAGATGCTGAAACTAAAGCTG
CAACCACCGCCGATCCCCTGAAAGCTCTGGACGAAGCCATCAGCTCCATCGACAAATTCC
GCTCCTCCCTCGGTGCGGTGCAGAACCGTCTGGATTCCGCGGTCACCAACCTGAACAACA
CCACTACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCTGACTATGCGACCGAAG
TATCCAACATGTCGAAAGCGCAGATCATCCAGCAGGCCGGTAACTCCGTGCTGGCAAAAG
CTAACCAGGTACCACAGCAGGTTCTGTCTCTGCTGCAGGTTAA

Figure 19

ATGGCACAAGTCATTAATACCAACAGC
CTCTCGCTGATCACTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATC
GAGCGTCTGTCTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCG
ATTGCTAACCGTTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAAC
GACGGTATTTCTGTTGCACAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTA
CAGCGTGTGCGTGAACTGACCGTTCAGGCAACCACCGGTACCAACTCCCAGTCTGACCTG
GACTCTATCCAGGACGAAATTAAATCCCGTCTGGACGAAATTGATCGCGTATCCGGTCAG
ACCCAGTTCAACGGCGTGAACGTGCTGGCAAAAGACGGTTCCATGAAAATTCAGGTTGGC
GCGAACGATGGCCAGACCATCACTATCGACCTGAAGAAGATTGACTCTTCTACCTTGAAC
CTGACAGGTTTTAACGTTAACGGTTCTGGTTCTGTGGCGAATACTGCAGCAACTAAAGCT
GATTTAACCGCTGCTCAACTCTCTGCACCGGGTGCAGCAGACGCAAATGGTACAGTTACT
TATACTGTCAGTGCTGGTTATAAAGAATCCACTGCTGCAGATGTTATTGCTAGCATCAAA
GACGGCAGTGCTCCGACTTCTGCAATTACTGCAACCATTAATAATGGCTTCGGTGATTCC
AGTGCGCTGACTTCCAATGACTATACTTATGACCCAGCAAAAGGCGACTTCACTTACGAC
GTAGCTTCAAGCGCCAATAATACTGCTGCCCAGGTTCAGTCCTTCCTGACGCCGAAAGCA
GGTGATACCGCAAATCTGAAAGTAACCGTTGGTACGACATCGGTTGATGTCGTTCTGGCC
AGTGATGGTAAGATTACAGCAAAAGATGGTTCTGCATTATATATCGACAGTACAGGTAAC
CTGACTCAGAACAGTGCTGGCTTGACCTCTGCTAAACTGGCTACTCTGACTGGCCTTCAG
GGCTCTGGTGTTGCTTCAACCATCACTACTGAAGATGGCACTAATATTGATATTGCTGCT
AACGGTAATATTGGTCTGACCGGTGTTCGTATCAGTGCTGATTCTCTGCAGTCAGCGACT
AAATCTACGGGCTTTACTGTTGGTACTGGCGCTACAGGTCTGACCGTAGGTACTGATGGT
AAAGTGACTATCGGCGGGACTACTGCTCAGTCCTACACCAGCAAAGATGGTTCCCTGACT
ACTGATAACACCACTAAACTGTATCTGCAGAAAGATGGCTCTGTAACCAACGGTTCAGGT
AAAGCGGTCTATGTAGAAGCGGATGGTGATTTCACTACCGACGCTGCAACCAAAGCCGCA
ACCACCACCGATCCGCTGAAAGCCCTGGATGAGGCAATCAGCCAGATCGATAAGTTCCGT
TCATCCCTGGGTGCTATCCAGAACCGTCTGGATTCCGCGGTCACCAACCTGAACAACACC
ACTACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTG
TCCAACATGTCGAAAGCGCAGATCATTCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCC
AACCAGGTACCGCAACAGGTTCTGTCTCTGCTGCAGGGCTAA

Figure 20

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCAC
TCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTC
TGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTT
TACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGT
TGCACAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTGTGCGTGA
ACTGACCGTTCAGGCAACCACCGGTACCAACTCCCAGTCTGACCTGGACTCTATCCAGGA
CGAAATTAAATCCCGTCTGGACGAAATTGATCGCGTATCCGGTCAGACCCAGTTCAACGG
CGTGAACGTGCTGGCAAAAGACGGTTCCATGAAAATTCAGGTTGGCGCGAACGATGGCCA
GACCATCACTATCGACCTGAAGAAGATTGACTCTTCTACCTTGAACCTGACAGGTTTTAA
CGTTAACGGTTCTGGTTCTGTGGCGAATACTGCAGCAACTAAAGCTGATTTAACCGCTGC
TCAACTCTCTGCACCGGGTGCAGCAGACGCAAATGGTACAGTTACTTATACTGTCAGTGC
TGGTTATAAAGAATCCACTGCTGCAGATGTTATTGCTAGCATCAAAGACGGCAGTGCTCC
GACTTCTGCAATTACTGCAACCATTAATAATGGCTTCGGTGATTCCAGTGCGCTGACTTC
CAATGACTATACTTATGACCCAGCAAAAGGCGACTTCACTTACGACGTAGCTTCAAGCGC
CAATAATACTGCTGCCCAGGTTCAGTCCTTCCTGACGCCGAAAGCAGGTGATACCGCAAA
TCTGAAAGTAACCGTTGGTACGACATCGGTTGATGTCGTTCTGGCCAGTGATGGTAAGAT
TACAGCAAAAGATGGTTCTGCATTATATATCGACAGTACAGGTAACCTGACTCAGAACAG
TGCTGGCTTGACCTCTGCTAAACTGGCTACTCTGACTGGCCTTCAGGGCTCTGGTGTTGC
TTCAACCATCACTACTGAAGATGGCACTAATATTGATATTGCTGCTAACGGTAATATTGG
TCTGACCGGTGTTCGTATCAGTGCTGATTCTCTGCAGTCAGCGACTAAATCTACGGGCTT
TACTGTTGGTACTGGCGCTACAGGTCTGACCGTAGGTACTGATGGTAAAGTGACTATCGG
CGGGACTACTGCTCAGTCCTACACCAGCAAAGATGGTTCCCTGACTACTGATAACACCAC
TAAACTGTATCTGCAGAAAGATGGCTCTGTAACCAACGGTTCAGGTAAAGCGGTCTATGT
AGAAGCGGATGGTGATTTCACTACCGACGCTGCAACCAAAGCCGCAACCACCACCGATCC
GCTGAAAGCCCTGGATGAGGCAATCAGCCAGATCGATAAGTTCCGTTCATCCCTGGGTGC
TATCCAGAACCGTCTGGATTCCGCGGTCACCAACCTGAACAACACCACTACCAACCTGTC
TGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAA
AGCGCAGATCATTCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCCAACCAGGTACCGCA
ACAGGTTCTGTCTCTGCTGCAGGGCTAA

Figure 21

GCGCTGTCGACTTCTATCGAGCGCCTCTCTTCTGGTCTGCGTATTAACAGCGCTAAA
GATGACGCTGCGGGCCAGGCGATTGCTAACCGCTTCACTTCTAACATCAAAGGTCTGACT
CAGGCCGCACGTAACGCCAACGACGGTATTTCTCTGGCGCAGACGGCTGAAGGCGCGCTG
TCAGAGATTAACAACAACTTGCAGCGTATTCGTGAACTGACCGTTCAGGCCTCTACCGGC
ACGAACTCTGATTCCGACCTGTCTTCTATTCAGGACGAAATCAAATCCCGTCTTGATGAA
ATTGACCGTGTATCTGGTCAGACCCAGTTCAACGGTGTGAACGTGCTGTCGAAAAACGAT
TCGATGAAGATTCAGATTGGTGCCAATGATAACCAGACGATCAGCATTGGCTTGCAACAA
ATCGACAGTACCACTTTGAATCTGAAAGGATTTACCGTGTCCGGCATGGCGGATTTCAGC
GCGGCGAAACTGACGGCTGCTGATGGTACAGCAATTGCTGCTGCGGATGTCAAGGATGCT
GGGGGTAAACAAGTCAATTTACTGTCTTACACTGACACCGCGTCTAACAGTACTAAATAT
GCGGTCGTTGATTCTGCAACCGGTAAATACATGGCAGCCACTGTAGTCATTACCAGTACG
GCGGCGGCGGTAACTGTTGGTGCAACGGAAGTGGCGGGAGCCGCTACAGCCGAACCGTTA
AAAGCACTGGATGCCGCAATCGCTAAAGTCGACAAATTCCGCTCCTCCCTCGGTGCCGTT
CAAAACCGTCTGGATTCTGCGGTCACCAACCTGAACAACACCACCACCAACCTGTCTGAA
GCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCG
CAGATTATCCAGCAGGCG

Figure 22

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAATA
ATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGC
GTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTTACTTCTA
ATATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAATGACGGTATTTCTGTTGCACAGA
CCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATTCGTGAACTGACGG
TTCAGGCCACTACAGGGACTAACTCCGATTCTGACCTGGACTCCATCCAGGACGAAATCA
AATCTCGTCTGGACGAAATTGACCGCGTATCCGGTCAGACCCAGTTCAACGGCGTGAACG
TGCTGTCCAAAGATGGTTCAATGAAAATTCAGGTCGGCGCAAATGATGGTGAAACCATCA
CGATTGATCTGAAGAAAATTGACTCTGATACGCTGAATCTGGCTGGTTTTAACGTGAATG
GCGAAGGTGAAACAGCCAATACTGCTGCAACACTTAAAGATATGGTTGGTTTAAAACTCG
ATAATACGGGGGTCACTACAGCTGGAGTTAATAGATATATTGCTGACAAAGCCGTCGCAA
GTAGCACGGATATTTTGAATGCGGTAGCTGGTGTTGATGGCAGTAAAGTTTCCACGGAGG
CAGATGTTGGTTTTGGTGCAGCTGCCCCTGGTACGCCAGTGGAATATACTTATCATAAAG
ATACTAACACATATACGGCTTCTGCTTCAGTTGATGCGACTCAACTGGCGGCATTCCTGA
ATCCTGAAGCGGGTGGTACCACTGCTGCAACAGTAAGTATTGGCAACGGTACAACAGCTC
AAGAGCAAAAAGTCATTATTGCTAAAGATGGTTCTTTAACTGCTGCTGATGACGGTGCCG
CTCTCTATCTTGATGATACTGGTAACTTAAGTAAAACTAACGCAGGCACTGATACTCAAG
CTAAACTGTCTGACTTAATGGCAAACAATGCTAATGCCAAAACAGTCATTACAACAGATA
AAGGTACATTTACTGCTAATACGACAAAGTTTGATGGGGTAGATATTTCTGTTGATGCTT
CAACGTTTGCTAACGCCGTTAAAAATGAGACTTACACTGCAACTGTTGGTGTAACTTTAC
CTGCGACATATACAGTCAATAATGGCACTGCTGCATCAGCGTATTTAGTCGATGGAAAAG
TGAGCAAAACTCCTGCCGAGTATTTTGCTCAAGCTGATGGCACTATTACTAGTGGTGAAA
ATGCGGCTACCAGTAAAGCTATCTATGTAAGTGCCAATGGTAACTTAACGACTAATACAA
CTAGTGAATCTGAAGCTACTACCAACCCGCTGGCAGCATTGGATGACGCTATCGCGTCTA
TCGACAAATTCCGTTCTTCCCTGGGTGCTATCCAGAACCGTCTGGATTCCGCAGTCACCA
ACCTGAACAACACCACTACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACT
ATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATCATTCAGCAGGCCGGTAACTCCG
TGCTGGCAAAAGCCAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 23

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAATAATAT
CAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGCGTAT
TAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTTACTTCTAACAT
TAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGTTGCGCAGACCAC
TGAAGGCGCGCTGTCCGAAATTAACAACAACTTACAGCGTATTCGTGAACTGACGGTTCA
GGCGACGACCGGAACTAACTCCACCTCTGACCTGGACTCCATCCAGGACGAAATCAAATC
CCGTCTTGACGAAATTGACCGCGTATCTGGTCAGACCCAGTTCAACGGCGTGAACGTGCT
GTCTAAAGATGGCTCGATGAAAATTCAGGTCGGCGCGAACGATGGCGAAACGATTACTAT
TGATCTGAAGAAAATTGACTCTGATACGCTGAATCTGGCTGGTTTTAACGTTAACGGTAA
AGGTTCTGTAGCGAATACCGCTGCGACTACAGATAATCTGACATTGGCTGGTTTTACAGC
GGGTACTAAAGCTGCTGATGGCACCGTAACTTATAGCAAAAATGTCCAGTTTGCCGCCGC
GACTGCAAGCAATGTACTGGCTGCTGCTAAAGATGGCGACGAAATTACGTTCGCTGGTAA
TAACGGCACAGGTATAGCTGCAACTGGGGGGACTTATACTTATCATAAGGACTCTAACTC
ATACAGCTTTAGCGCAACGGCTGCATCTAAAGATTCTCTGTTGAGCACACTGGCACCAAA
CGCTGGCGATACATTTACCGCTAAAGTGACTATTGGTTCTAAATCGCAAGAAGTTAACGT
TAGCAAAGATGGTACGATTACATCCAGCGATGGTAAGGCGCTGTATTTAGATGAGAAGGG
CAACCTGACCCAAACAGGTAGTGGCACAACCAAAGCTGCAACCTGGGATAACCTGATGGC
CAATACAGATACTACAGGCAAAGATGCCTATGGTAACTCTGCGGCAGCAGCTGTTGGGAC
AGTAATCGAAGCAAAAGGAATGACCATCACTTCTGCTGGTGGTAATGCTCAGGTGTTAAA
AGACGCGGCTTATAATGCCGCATATGCGACCTCAATTACTACTGGTACTCCGGGTGATGC
GGGAGCCGCGGGAGCCGCTGCAACTGCGGGTAATGCCGCGGTGGGAGCGCTGGGCGCAAC
GGCAGTTGATAATACCACGGCAGATGTTGCCGATATCTCTATCTCAGCTTCGCAAATGGC
GAGCATCCTTCAGGATAAAGATTTCACCTTAAGTGATGGTAGTGATACTTACAACGTGAC
CAGCAATGCTGTCACTATCAATGGCAAAGCAGCAAACATTGATGACAGCGGCGCAATCAC
AGACCAAACCAGTAAAGTTGTCAATTATTTCGCTCATACTAACGGTAGCGTGACTAACGA
TACAGGCTCCACTATTTATGCGACAGAAGATGGTAGCCTGACCACCGATGCAGCAACCAA
AGCCGAAACCACCGCCGATCCCCTGAAAGCTCTGGACGAAGCCATCAGCTCCATCGACAA
ATTCCGCTCCTCCCTCGGTGCGGTGCAAAACCGTCTGGATTCCGCGGTCACCAACCTGAA
CAACACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGAC
CGAAGTGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCCGGTAACTCCGTGCTGGC
AAAAGCTAACCAGGTACCACAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 24

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTG
ATCACTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTG
TCTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAAC
CGTTTTACTTCTAACATTAAAGGCCTGACTCAGGCGGCCCGTAACGCCAACGACGGTATT
TCTGTTGCGCAGACCACCGAAGGCGCGCTGTCCGAAATTAACAACAACTTACAGCGTGTG
CGTGAGCTGACTGTTCAGGCGACCACCGGTACCAACTCCCAGTCTGATCTGGACTCTATC
CAGGACGAAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCCGGTCAGACCCAGTTC
AACGGCGTGAACGTGCTGGCAAAAGACGGTTCCATGAAAATTCAGGTTGGCGCGAATGAT
GGCCAGACCATCACTATCGACCTGAAGAAGATTGACTCTTCTACGTTGAAACTGACTGGT
TTTAACGTGAATGGTTCTGGTTCTGTGGCGAATACTGCGGCGACTAAAGCGGATTTGGCT
GCTGCTGCAATTGGTACCCCTGGGGCAGCAGATTCTACAGGTGCCATTGCTTACACAGTA
AGTGCTGGGCTGACTAAAACTACAGCCGCAGATGTACTGTCTAGCCTCGCTGATGGTACG
ACTATTACAGCCACAGGCGTGAAAAATGGCTTTGCTGCAGGAGCCACTTCCAATGCCTAT
AAACTTAACAAAGATAATAATACATTTACTTATGACACGACTGCTACGACAGCTGAGCTG
CAGTCTTACCTGACTCCGAAAGCGGGCGACACTGCAACATTCAGTGTTGAAATTGGTGGT
ACTACACAAGACGTCGTGCTGTCCAGTGATGGCAAACTCACTGCTAAGGATGGCTCTAAG
CTTTACATTGATACAACTGGTAATTTAACTCAGAATGGTGGTAATAACGGTGTTGGAACA
CTCGCGGAAGCGACTCTGAGTGGTTTAGCTCTGAACAAAAATGGTTTAACGGCTGTTAAA
TCCACAATTACTACAGCTGATAACACTTCGATTGTACTGAATGGTTCAAGCGATGGTACT
GGTAATGCTGGTACTGAAGGTACGATTGCTGTTACAGGCGCTGTAATTAGTTCAGCTGCT
CTGCAATCTGCAAGCAAAACGACTGGTTTCACTGTTGGTACAGTAGACACAGCTGGTTAT
ATCTCTGTAGGTACTGATGGGAGTGTTCAGGCATATGATGCTGCGACTTCTGGCAACAAA
GCTTCTTACACCAACACTGACGGTACACTGACTACTGATAACACCACTAAACTGTATCTG
CAGAAAGATGGCTCTGTAACCAACGGTTCAGGTAAAGCGGTCTATGTAGAAGCGGATGGT
GATTTCACTACCGACGCTGCAACCAAAGCCGCAACCACCACCGATCCGCTGGCCGCTCTG
GATGACGCAATCAGCCAGATCGACAAGTTCCGTTCATCCTTGGGTGCTATCCAGAACCGT
CTGGATTCTGCAGTCACCAACCTGAACAACACCACCACCAACCTGTCTGAAGCGCAGTCC
CGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAATATGTCGAAAGCGCAGATCATC
CAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCCAACCAGGTACCGCAGCAGGTTCTGTCT
CTGCTGCAGGGTTAA

Figure 25

AACAAATCTCAGTCTTCTCTGAGCTCCGCCATTGAA
GGTCTCTCTTCTGGCCTGCGTATTAACAGTGCTAAAGATGACGCAGCAGGTCAGGCGATT
GCTAACCGTTTTACAGCAAATATTAAAGGTCTGACTCAGGCTTCCCGTAACGCGAATGAT
GGTATTTCTGTTGCGCAGACCACTGAAGGTGCGCTGAATGAAATTAACAACAACCTGCAG
CGTATTCGTGAACTTTCTGTTCAGGCAACTAACGGTACTAACTCTGACAGCGATCTTTCT
TCTATCCAGGCTGAAATTACTCAACGTCTGGAAGAAATTGACCGTGTATCTGAGCAAACT
CAGTTTAACGGCGTGAAAGTCCTTGCTGAAAATAATGAAATGAAAATTCAGGTTGGTGCT
AATGATGGTGAAACCATCACTATCAATCTGGCAAAAATTGATGCGAAAACTCTCGGCCTG
GACGGTTTTAATATCGATGGCGCGCAGAAAGCAACCGGCAGTGACCTGATTTCTAAATTT
AAAGCGACAGGTACTGATAATTATCAAATTAACGGTACTGATAACTATACTGTTAATGTA
GATAGTGGCGTAGTACAGGATAAAGATGGCAAACAAGTTTATGTGAGTACTGCGGATGGT
TCACTTACGACCAGCAGTGATACTCAATTCAAGATTGATGCAACTAAGCTTGCAGTGGCT
GCTAAAGATTTAGCTCAAGGGAATAAGATTGTCTACGAAGGTATCGAATTTACAAATACC
GGCACTGTCGCTATAGATGCCAAAGGTAATGGTAAATTAACCGCCAATGTTGATGGTAAG
GCTGTTGAATTCACTATTTCGGGGAGTACTGATACATCAGGTACTAGTGCAACCGTTGCC
CCTACGACAGCCCTATACAAAAATAGTGCAGGGCAATTGACTGCAACAAAAGTTGAAAAT
AAAGCAGCGACACTATCTGATCTTGATCTGAACGCTGCCAAGAAAACAGGAAGCACGTTA
GTTGTTAACGGTGCAACTTACGATGTTAGTGCAGATGGTAAAACGATAACGGAGACTGCT
TCTGGTAACAATAAAGTCATGTATCTGAGCAAATCAGAAGGTGGTAGCCCGATTCTGGTA
AACGAAGATGCAGCAAAATCGTTGCAATCTACCACCAACCCGCTCGAAACTATCGACAAA
GCATTGGCTAAAGTTGACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACCGTTTCGAC
TCTGCCATCACCAACCTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTAGCCGTATC
GAAGATGCTGACTACGCGACCGAAGTGTCTAACATGTCTCGTGCGCAGATCCTGCAACAA
GCGGGTACCTCTGTTCTGGCACAG

Figure 26

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAATA
ATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGC
GTATTAACAGCGCGAAGGATGACGCAGCGGGTCAGGCGATTGCTAACCGTTTTACTTCTA
ACATTAAAGGCCTGACTCAGGCGGCACGTAACGCCAACGACGGTATCTCTCTGGCGCAGA
CCACCGAAGGTGCGCTGTCTGAAATCAACAACAACTTACAGCGTGTACGTGAACTGACCG
TTCAGGCAACCACCGGTACTAACTCCGACTCCGACCTGGCTTCTATTCAGGACGAAATCA
AATCCCGTCTGGATGAAATTGACCGCGTATCTGGTCAGACTCAGTTCAACGGCGTGAACG
TGCTGGCAAAAGACGGTTCCATGAAAATTCAGGTAGGTGCTAACGACGGCCAGACTATCA
CTATTGACCTGAAAAAAATCGACTCTGATACTCTGGGCCTGAATGGTTTTAACGTGAATG
GTTCTGGGACGATTACCAACAAAGCAGCAACTGTCAGTGATGTTACTCGCGCAGGCGGTA
CATTGGTGAATGGTGCCTATGATATAAAAACCACTAACACAGCGCTGACTACAACTGATG
CCTTCGCGAAATTGAATGATGGTGATGTTGTTACTATCAATAATGGTAAGGATACTGCCT
ATAAATATAATGCTGCTACAGGTGGGTTTACGACGGATGTCTCCATCTCCGGGGATCCTA
CCGCTGCTGACGCTACTGCTAATAAAACTGCCCGTGATGCACTTGCGGCGTCTTTACATG
CTGAGCCGGGTAAAACTGTTAATGGTTCTTGGACTACGAATGATGGTACGGTAAAATTTG
ATACCGATGCCGATGGTAAGATTTCTATTGGTGGTGTTGCTGCTTATGTAGATGCAGCAG
GCAACCTGACCACTAACGCAGCAGGTATGACGACTCAAGCAACAACTACCGATTTGGTTA
CTGCTGCTGCATCTGCTACTGGTAAGGGTGGATCCCTGACCTTTGGTGACACGACGTATA
AAATTGGTCAGGGTACGGCTGGGGTTGATCCTGATGACGCTTCAGATGATGTACTGGGCA
CCATTTCTTACTCTAAATCAGTAAGCAAGGATGTTGTTCTTGCTGATACTAAAGCAACTG
GTAACACGACAACAGTTGATTTCAACTCCGGTATCATGACTTCAAAGGTTAGTTTCGATG
CAGGTACATCAACTGATACATTCAAAGATGCAGATGGTGCTATCACCAAAACTAAAGAAT
ACACCACTTCTTATGCTGTAAATAAAGATACTGGTGAAGTTACCGTTGCTGATTATGCTG
CGGTAGATAGCGCCGATAAGGCTGTTGATGATACTAAATATAAACCGACTATCGGCGCGA
CAGTTAACCTGAATTCTGCAGGTAAATTGACCACTGATACCACCAGTGCAGGCACAGCAA
CCAAAGATCCTCTGGCTGCCCTGGACGCTGCTATCAGCTCCATCGACAAATTCCGTTCAT
CCCTGGGTGCTATCCAGAACCGTCTGGATTCCGCAGTCACCAACCTGAACAACACCACTA
CCAACCTGTCCGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCA
ACATGTCGAAAGCGCAGATTATCCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCCAACC
AGGTACCGCAGCAGGTTCTGTCTCTGCTACAGGGTTAA

Figure 27

AACAAAAACCAGTCTGCGCTGTCGACTTCTATC
GAGCGCCTTTCTTCTGGTCTGCGTATTAACAGCGCTAAAGATGACGCTGCGGGCCAGGCG
ATTGCTAACCGCTTCACTTCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAAC
GACGGTATTTCTCTGGCGCAGACCACTGAAGGCGCGCTGTCTGAGATTAACAACAACTTG
CAGCGTGTGCGTGAGTTGACTGTACAGGCGACGACCGGGACTAACTCTGATTCTGACCTG
TCTTCTATCCAGGATGAAATCAAATCCCGTTTAAGCGAAATTGACCGTGTATCTGGTCAG
ACTCAGTTTAACGGCGTGAACGTACTGGCTAAGAATGACACCCTGTCTATTCAGGTAGGT
GCAAATGACGGTCAGACTATCAATATTGACCTGCAGCAAATCGATTCTCATACACTGGGT
CTGGATGGTTTCAGCGTTAAAAATAATGATGCAGTGAAAACCAGTGCTGCCGTGAATACT
CTTGGGGGGGGGCAGGTTCTGTTGCTGTCGACTTCGCAACAACCAGTTTGACTGCTATC
ACTGGTCTCGGTAGCGGTGCTATCAGCGAAATTGCTAAAGACGATAATGGTGATTACTAC
GCGCATGTCACAGGGACTACGGGTAATACTGCTGATGGTTACTATGCTGTCGATATCGAC
AAGGCTACCGGTGAGGTCGCTCTGAAAGATGGTAACGTAGATACACCGACAGGTACGCCA
ACGACGACAAGCACATATGACTTCACAGACGCTGGTCAAACCGTTTCCTTTGGCACTGAT
GCTGCAACAGCCGGTATCAGCACTGGTGCTTCTCTCGTTAAACTTCAGGATGAGAAAGGC
AATGATACTGCTACTTATGCAATCAAAGCACAAGATGGCAGCCTGTATGCCGCCAACGTT
GATGAGGCTACCGGTAAAGTCACTGTCAAAACCGCCAGCTATACTGATGCTGACGGCAAA
GCAGTGACCGATGCCGCTGTAAAACTGGGTGGTGACAATGGCACAACCGAAATTGTTGTC
GATGCTGCGTCAGGTAAAACTTACGATGCTGGTGCACTGCAAAACGTTGATCTCTCCAGT
GCAACCAACACGGTAACCGCAATCCCGAACGGTAAAACCACGTCTCCGCTGGCTGCCCTT
GACGACGCAATCAGCCAGATCGACAAATTCCGCTCCTCCCTCGGTGCGGTGCAGAACCGT
CTGGATTCCGCGGTCACCAACCTGAACAACACCACTACCAACCTGTCTGAAGCGCAGTCC
CGTATTCAGGACGCTGACTATGCGACCGAAGTATCCAACATGTCGAAAGCGCAGATCATC
CAGCAGGCAGGTAACTCCGTGCTGTCCAAA

Figure 28

GCGCTGTCGACTTCTATCGAGCGCCTCTCTTCTGGTCTGCGCATTAACAGCGCTAAAG
ATGACGCTGCGGGCCAAGCGATTGCTAACCGCTTCACTTCTAACATCAAAGGTCTGACTC
AGGCCGCACGTAACGCCAACGACGGTATTTCTCTGGCGCAGACCACTGAAGGCGCACTGT
CTGAAATCAACAACAACTTGCAGCGTGTTCGTGAACTGACCGTTCAGGCCACTACCGGTA
CTAACTCTGATTCTGACCTGTCTTCAATACAGGACGAAATCAAATCCCGTCTCGATGAAA
TTGACCGCGTATCCGGTCAGACTCAGTTCAACGGCGTTAATGTTCTTTCCAAAGATGGTT
CAATGAAAATTCAGGTTGGTGCGAATGATGGTCAAACTATCTCCATCGATCTGAAGAAAA
TTGATTCTTCAACTTTGGGGCTGAATGGCTTCTCAGTTTCTAAAAACTCTCTTAATGTCA
GCAATGCTATCACATCTATCCCGCAAGCCGCTAGCAATGAACCTGTTGATGTTAACTTCG
GTGATACTGATGAGTCTGCAGCAATCGCAGCCAAATTGGGGGTTTCCGATACGTCAAGCC
TGTCGCTGCACAACATCCTTGATAAAGATGGTAAGGCAACAGCTGATTATGTTGTTCAGT
CAGGTAAAGACTTCTATGCTGCTTCTGTTAATGCCGCTTCAGGTAAAGTAACCTTAAACA
CCATTGATGTTACTTATGATGATTATGCGAACGGTGTTGACGATGCCAAGCAAACAGGTC
AGCTGATCAAAGTTTCAGCAGATAAAGACGGCGCAGCTCAAGGTTTTGTCACACTTCAAG
GCAAAAACTATTCTGCTGGTGATGCGGCAGACATTCTTAAGAATGGAGCAACAGCTCTTA
AGTTAACTGATCTGAATTTAAGTGATGTTACTGATACTAATGGTAAGGTAACCACAACTG
CGACTGAGCAATTTGAAGGTGCTTCAACTGAGGATCCGCTGGCGCTTCTGGATAAAGCTA
TTGCATCAGTCGACAAATTCCGGTCTTCTCTAGGTGCCGTGCAGAACCGTCTCGATTCCG
CTATCACCAACCTGAACAACACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGG
ACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATCATCCAGCAGGCA

Figure 29

ATGGCACAAGTCATTAATACCAACAGCCTCTCG
CTGATCACTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGT
CTGTCTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCT
AACCGTTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGT
ATTTCTGTTGCACAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGT
ATTCGTGAACTGACGGTTCAGGCCACTACAGGGACTAACTCCGATTCTGACCTGGACTCC
ATCCAGGACGAAATCAAATCTCGTCTGGACGAAATTGACCGCGTATCTGGTCAGACCCAG
TTCAACGGCGTGAACGTGCTGTCTAAAGATGGCTCGATGAAAATTCAGGTCGGCGCGAAC
GATGGCGAAACGATTACTATTGATCTGAAGAAAATTGACTCTGATACGCTAAATCTGGCT
GGTTTTAACGTGAATGGTGCTGGCTCTGTTGATAATGCCAAGGCGACTGGCAAAGATCTT
ACTGATGCTGGTTTTACGGCAAGCGCAGCTGATGCTAATGGCAAAATCACTTATACCAAA
GACACCGTTACTAAATTCGACAAAGCGACAGCGGCTGATGTATTGGGCAAAGCGGCTGCT
GGCGATAGCATTACCTATGCGGGCACTGATACTGGCTTAGGAGTCGCTGCTGATGCCTCG
ACTTACACCTACAATGCAGCCAATAAGTCTTACACTTTTGATGCTACTGGTGTTGCCAAG
GCGGATGCTGGAACGGCACTGAAAGGGTACTTAGGCGCATCTAACACCGGTAAAATTAAT
ATCGGTGGTACCGAGCAAGAAGTTAACATTGCCAAAGATGGCTCCATCACCGATACCAAT
GGCGATGCGCTGTATCTCGATAGTACCGGCAACTTAACCAAAAATACCGCGAATTTGGGG
GCTGCTGATAAAGCAACTGTAGATAAACTGTTTGCTGGTGCTCAGGATGCAACGATCACC
TTCGATAGCGGCATGACAGCTAAATTCGATCAAACTGCTGGTACCGTTGATTTCAAAGGC
GCGTCTATTTCTGCTGATGCAATGGCATCAACCTTAAATAATGGTTCCTATACAGCCAAC
GTAGGTGGTAAGGCTTATGCCGTAACCGCTGGCGCAGTTCAGACAGGTGGCGCAGATGTG
TATAAAGATACCACTGGCGCACTGACGACTGAAGATGACGAAACCGTTACCGCGACCTAC
TACGGTTTTGCTGATGGTAAAGTTTCTGACGGTGAAGGTTCTACTGTCTATAAAGCTGCT
GATGGTTCCATCACTAAAGATGCGACTACCAAGTCTGAAGCAACCACTGACCCTCTGAAA
GCCCTTGACGACGCAATCAGCCAGATCGACAAATTCCGCTCCTCCCTCGGTGCCGTTCAA
AACCGTCTGGATTCCGCCGTCACCAACCTGAACAACACCACTACCAACCTGTCTGAAGCG
CAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAG
ATCATTCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCCAACCAGGTACCGCAGCAGGTT
CTGTCTCTGCTGCAGGGTTAA

Figure 30

AACAAATCTCAGTCTTCTCTTAGCTCTGCTATTGA
GCGTCTCTCTTCTGGCCTGCGTATTAACAGTGCTAAAGATGACGCAGCAGGTCAGGCGAT
TGCTAACCGTTTTACGGCAAATATTAAAGGTCTGACTCAGGCTTCCCGTAACGCGAATGA
TGGTATTTCTGTTGCGCAGACTACTGAAGGTGCGCTGAATGAAATTAACAACAACCTGCA
GCGTGTACGTGAACTGACTGTTCAGGCAACTAACGGTACTAACTCTGACAGCGATCTTTC
TTCTATTCAGGCAGAAATTACTCAACGTCTGGAAGAAATTGACCGTGTATCTGAGCAAAC
TCAGTTTAACGGCGTGAAAGTCCTTGCCGAAAATAATGAAATGAAAATTCAGGTTGGTGC
TAATGATGGGGAAACCATCACTATCAATCTGGCAAAAATTGATGCGAAAACTCTCGGCCT
GGACGGCTTTAATATCGATGGCGCGCAGAAAGCAACTGGCAGTGACCTGATTTCTAAATT
TAAAGCGACAGGTACTGATAATTATCAAATTAACGGTACTGATAACTATACTGTTAATGT
AGATAGTGGAGCAGTTCAAAATGAGGATGGTGACGCAATTTTTGTTAGCGCTACCGATGG
TTCTCTGACTACTAAGAGTGATACAAAAGTCGGTGGTACAGGTATTGATGCGACTGGGCT
TGCAAAAGCCGCAGTTTCTTTAGCTAAAGATGCCTCAATTAAATACCAAGGTATTACTTT
CACCAACAAAGGCACTGATGCATTTGATGGCAGTGGTAACGGCACTCTAACCGCTAATAT
TGATGGCAAAGATGTAACCTTTACTATTGATGCGACAGGGAAGGACGCAACATTAAAAAC
GTCTGATCCTGTTTACAAAAATAGTGCAGGTCAGTTCACTACAACTAAGGTTGAAAACAA
AGCCGCTACAGCATCGGATCTGGACTTAAATAACGCTAAAAAAGTGGGTAGTTCTTTAGT
TGTAAATGGCGCTGATTATGAAGTTAGCGCTGATGGTAAGACAGTAACTGGGCTTGGCAA
AACTATGTATCTGAGCAAATCAGAAGGTGGTAGCCCGATTCTGGTAAAAGAAGATGCAGC
AAAATCGTTGCAATCTACTACCAACCCGCTCGAAACCATCGACAAGGCATTGGCTAAAGT
TGACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACCGTTTCGACTCTGCTATCACCAA
CCTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTAGCCGTATCGAAGATGCTGACTA
CGCGACCGAAGTGTCTAACATGTCTCGTGCGCAGATCCTGCAACAAGCGGGTACCTCTGT TCTGGCGCAG

Figure 31

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAATA
ATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGC
GTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTTACTTCTA
ACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGATGGTATTTCTGTTGCACAGA
CCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATCCGTGAACTGACGG
TTCAGGCTTCTACCGGGACTAACTCCGATTCGGATCTGGACTCCATTCAGGACGAAATCA
AATCCCGTCTGGACGAAATTGACCGCGTATCTGGCCAGACCCAGTTCAACGGCGTGAACG
TACTGGCGAAAGACGGTTCAATGAAAATTCAGGTTGGTGCGAATGACGGCCAGACTATCA
CGATTGATCTGAAGAAAATTGACTCTGATACGCTGGGGCTGAGTGGGTTTAATGTGAATG
GTAGCGGGGCTGTGGCTAATACTGCAGCGACTAAATCTGATTTGGCAGCAGCTCAACTCT
TGGCTCCAGGTACTGCTGATGCTAATGGTACAGTTACCTATACTGTTGGCGCAGGCCTGA
AAACATCTACAGCTGCAGATGTAATTGCGAGTTTGGCTAATAACGCAAAAGTTAATGCCA
CAATTGCAAATGGTTTTGGATCGCCAACAGCTACAGATTATACATACAACAGCGCTACAG
GCGATTTTACATATAGTGCAACTATTGCAGCTGGTACAAATTCTGGTGATAGTAACAGTG
CTCAGTTACAATCCTTCCTGACACCAAAAGCGGGCGATACTGCTAACTTAAACGTTAAAA
TTGGTTCTACGTCAATTGACGTTGTATTGGCTAGCGACGGTAAAATTACCGCGAAAGATG
GTTCAGAACTATTTATTGACGTAGATGGTAACCTCACTCAAAACAATGCTGGGACTGTCA
AAGCAGCCACTCTTGATGCACTGACTAAAAACTGGCATACAACAGGCACACCGAGTGCCG
TATCTACGGTAATTACAACTGAAGATGAAACAACCTTCACTCTGGCTGGCGGTACTGATG
CTACTACTTCTGGTGCAATCACTGTAGCAAATGCAAGAATGAGTGCTGAGTCTCTTCAAT
CGGCAACTAAGTCCACAGGATTCACAGTTGATGTTGGAGCTACTGGTACCAGCGCAGGCG
ATATTAAAGTTGATAGTAAAGGTATAGTACAACAACACACAGGTACAGGTTTTGAAGACG
CTTACACCAAAGCTGATGGTTCACTGACTACCGATAATACAACCAATCTGTTTTTGCAAA
AAGACGGAACTGTGACCAATGGTTCAGGTAAAGCAGTCTATGTTTCAGCGGATGGTAATT
TTACTACTGACGCTGAAACTAAAGCTGCAACCACCGCCGATCCACTGAAAGCTCTGGACG
AAGCGATCAGCTCCATCGACAAATTCCGTTCTTCCCTCGGTGCGGTGCAAAACCGTCTGG
ATTCCGCAGTCACCAACCTGAACAACACCACTACTAACCTGTCTGAAGCGCAGTCCCGTA
TTCAGGACGCTGACTATGCGACCGAAGTGTCCAATATGTCGAAAGCGCAGATCATCCAGC
AGGCCGGTAACTCCGTGCTGGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTGTCTCTGC TGCAGGGTTAA

Figure 32

AACAAAAACCAGTCTGCGCTGTCGACTTCTATCGAGCGCCTCTCTT
CTGGTCTGCGCATTAACAGCGCTAAAGATGACGCTGCGGGCCAGGCGATTGCTAACCGCT
TCACTTCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAACGACGGTATCTCTC
TGGCGCAGACCACTGAAGGCGCACTGTCTGAAATCAACAACAACTTGCAGCGTGTTCGTG
AGCTGACCGTTCAGGCCACTACCGGTACTAACTCTGATTCTGACCTGTCTTCAATCCAGG
ACGAAATCAAATCCCGTCTCGATGAAATTGACCGCGTATCCGGTCAGACTCAGTTCAACG
GCGTGAACGTACTGGCAAAAGATAACACCATGAAGATTCAGGTTGGTGCGAACGATGGTC
AGACTATATCCATCGACCTGCAAAAAATCGACTCTTCTACTCTTGGTTTGAACGGTTTCT
CCGTTTCTAAAAATGCTCTCGAAACTAGCGAAGCGATCACTCAGTTGCCGAACGGTGCGA
ATGCACCAATCGCTGTGAAGATGGATGCGTCTGTTCTGACCGATCTTAACATTACTGATG
CTTCCGCTGTTTCGCTGCACAACGTAACTAAAGGTGGTGTCGCAACGTCTACTTATGTTG
TTCAGTATGGCGATAAGAGCTATGCAGCATCTGTTGATGCGGGAGGTACAGTAAAACTGA
ATAAAGCCGACGTAACATATAACGACGCAGCAAATGGTGTTACGAATGCCACCCAGATTG
GTAGTCTGGTTCAGGTTGGTGCTGATGCAAACAATGATGCAGTTGGTTTTGTTACCGTGC
AGGGGAAAAACTATGTTGCTAATGACTCATTAGTCAATGCTAATGGCGCTGCTGGCGCTG
CAGCAACTAGAGTTACAATTGATGGTGATGGTAGCCTTGGAGCTAACCAGGCTAAAATTG
AACTTAGCCAAAATGGTGCTACTGCTGCAACATCAGAGTTCGCTGGTGCTTCAACCAACG
ATCCACTGACTCTGCTGGACAAAGCTATCGCATCTGTTGATAAATTCCGTTCTTCTTTGG
GGGCGGTACAGAACCGTCTGAGCTCCGCTGTAACCAACCTGAACAACACCACTACCAACC
TGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAACATGT
CGAAAGCGCAGATCATCCAGCAGGCAGGTAACTCCGTGCTGTCCAAA

Figure 33

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAATAATATCAACAAGA
ACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGCGTATTAACAGCG
CGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTTACTTCTAACATTAAAGGCC
TGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGTTGCACAGACCACTGAAGGCG
CGCTGTCCGAAATCAACAACAACTTACAGCGTATTCGTGAACTGACGGTTCAGGCGACGA
CCGGAACTAACTCCACCTCTGACCTGGACTCCATTCAGGACGAAATCAAATCCCGTCTTG
ATGAAATTGACCGCGTATCCGGCCAAACCCAGTTCAACGGCGTGAACGTACTGTCAAAAG
ATGGCTCGATGAAAATTCAGGTCGGCGCAAATGATGGTGAAACCATCACGATTGATCTGA
AAAAGATCGACTCTTCTACATTGAAGCTGACCAGCTTCAATGTTAACGGTAAAGGCGCTG
TTGATAATGCTAAAGCCACTGAAGCAGATCTGACCGCTGCGGGCTTCTCCCAAGGTGCAG
TCGTCAGTGGCAACAGCACCTGGACTAAATCTACTGTTACTACCTTTAATGCAGCAACAG
CTACCGACGTGCTGGCAAGCGTTAGCGGCGGCAGCACTATTAGCGGTTATACCGGTACAA
ACAATGGATTAGGCGTAGCGGCTTCTACTGCATATACCTACAACGCAACCAGCAAGTCTT
ATTCATTTGACGCAACCGCACTTACCAATGGCGATGGTACTGGGGCCACCACTAAAGTTG
CTGATGTGCTGAAAGCCTATGCAGCAAACGGTGATAATACGGCTCAGATCTCCATCGGCG
GAAGCGCTCAGGACGTTAAAATTGCCAGCGATGGCACCCTGACTGACGTCAATGGTGATG
CTTTATATATTGGTTCTGACGGCAACCTGACTAAAAACCAGGCCGGCGGTCCAGATGCGG
CAACGTTGGACGGTATTTTCAACGGTGCGAATGGTAATGCAGCAGTTGATGCGAAGATTA
CATTCGGCAGCGGCATGACCGTTGATTTCACCCAGGCTAGCAAAAAAGTGGATATTAAGG
GCGCAACGGTATCCGCCGAAGATATGGACACTGCGTTAACTGGGCAGGCTTATACCGTAG
CTAACGGCGCACAGTCTTTTGACGTTGCCGCTGGTGGGGCAGTAACCGCTACTACAGGTG
GCGCTACCGTAAATATTGGTGCTGATGGTGAACTGACGACTGCGACCAACAAGACTGTCA
CAGAAACTTATCACGAATTTGCTAACGGCAATATTCTGGATGATGACGGCGCGGCTCTGT
ACAAAGCGGCTGACGGTTCTCTGACCACTGAAGCTACTGGTAAATCCGAAGTGACCACGG
ATCCGCTGAAAGCGCTGGACGATGCTATCGCATCCGTAGACAAATTCCGCTCCTCCCTCG
GTGCGGTGCAGAACCGTCTGGATTCCGCAGTCACCAACCTGAACAACACCACTACCAACC
TGTCTGAAGCGCAGTCCCGCATTCAGGACGCCGACTATGCGACCGAAGTGTCCAATATGT
CGAAAGCGCAGATCATCCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCCAACCAGGTAC
CGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 34

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCAG
TCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTC
TGGCTTGCGTATTAACAGCGCTAAGGATGACGCCGCGGGTCAGGCGATTGCTAACCGTTT
TACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGT
TGCGCAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATCCGTGA
ACTGACGGTTCAGGCTTCTACCGGGACTAACTCCGATTCGGATCTGGACTCCATTCAGGA
CGAAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCTGGCCAGACCCAGTTCAACGG
CGTGAACGTACTGGCGAAAGACGGTTCAATGAAAATTCAGGTTGGTGCGAATGACGGCCA
GACTATCACTATTGATCTGAAGAAAATTGACTCAGATACGCTGGGGCTGAGTGGGTTTAA
TGTGAATGGTGGCGGGGCTGTTGCTAATACTGCAGCGACTAAAGATGATTTGGTCGCTGC
ATCAGTTTCAGCTGCGGTAGGTAATGAATACACTGTCTCTGCTGGCCTGTCGAAATCAAC
TGCTGCTGATGTTATTGCTAGTCTCACAGATGGTGCGACAGTAACTGCGGCTGGTGTAAG
CAATGGTTTTGCTGCAGGGGCAACTGGAGATGCTTATAAATTCAATCAAGCAAACAACAC
TTTTACTTACAATACCACCTCAACAGCGGCAGAACTCCAATCTTACCTCACGCCTAAGGC
GGGGGATACCGCAACTTTCTCCGTTGAAATTGGTGGCACCAAGCAGGATGTTGTTCTGGC
TAGTGATGGCAAAATCACAGCAAAAGACGGGTCTAAACTTTATATTGACACCACAGGGAA
TTTAACCCAAAACGGTGGAGGTACTTTAGAAGAAGCTACCCTCAATGGCTTAGCTTTCAA
CCACTCTGGTCCAGCCGCTGCTGTACAATCTACTATTACTACTGCGGATGGAACTTCAAT
AGTTCTAGCAGGTTCTGGCGACTTTGGAACAACAAAAACTGCTGGGGCTATTAATGTCAC
AGGAGCAGTGATCAGTGCTGATGCACTTCTTTCCGCCAGTAAAGCGACTGGGTTTACTTC
TGGCACTTATACCGTAGGTACAGATGGAGTTGTTAAATCTGGTGGCAATGACGTTTATAA
CAAAGCTGACGGGACGGGATTAACTACTGACAATACCACAAAATATTATTTACAAGATGA
CGGGTCTGTAACTAATGGTTCTGGTAAAGCTGTGTATGCTGATGCAACAGGAAAACTAAC
TACTGACGCTGAAACTAAAGCCGAAACCACCGCCGATCCCCTGAAAGCTCTGGACGAAGC
GATCAGCTCCATCGACAAATTCCGTTCTTCCCTCGGTGCGGTGCAAAACCGTCTGGATTC
CGCGGTCACCAACCTGAACAACACCACTACCAACCTGTCCGAAGCGCAGTCCCGTATTCA
GGACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATCATCCAGCAGGC
CGGTAACTCCGTGCTGGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGCA GGGTTAA

Figure 35

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCAC
TCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTC
TGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCGGGTCAGGCGATTGCTAACCGTTT
TACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCCGT
TGCGCAGACCACCGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATCCGTGA
ACTGACGGTTCAGGCCACTACCGGTACTAACTCCGATTCTGACCTGGACTCCATCCAGGA
CGAAATCAAATCTCGTCTTGATGAAATTGACCGCGTATCTGGTCAGACCCAGTTCAATGG
CGTGAATGTGTTGTCCAAAGACGGTTCAATGAAAATTCAGGTGGGCGCAAATGATGGTGA
AACCATCACGATTGACCTGAAAAAAATCGACTCTTCTACACTGAAGCTGACCAGCTTCAA
CGTCAACGGTAAAGGCGCTGTTGATAATGCAAAAGCCACTGAAGCAGATCTGACCGCTGC
GGGCTTCTCCCAAAGTGCAGTTGTCAGTGGCAATAGCACCTGGACTAAATCTACTGTTAC
TACCTTTAATGCAGCAACAGCTACCGATGTGCTGGCTAGCGTTAGTGGCGGCAGCACTAT
TAGCGGTTATGCTGGCACAAACAATGGGTTAGGCGTAGCGGCTTCTACTGCATATACCTA
CAACGCAACCAGCAAGTCTTATTCATTTGACGCAACCGCACTTACTAATGGTGATGGTAC
TGCGGGCTCAACTAAAGTTGCTGATGTTCTGAAAGCCTATGCAGCAAACGGCGATAACAC
GGCTCAGATCTCCATCGGTGGTAGCGCTCAGGAAGTTAAAATTGCCAGCGATGGTACCCT
GACGGATACTAATGGCGATGCTTTATACATTGGTGCTGACGGTAACCTGACGAAAAACCA
GGCCGGCGGCCCAGCCGCGGCAACGTTGGACGGTATTTTCAACGGTGCGAATGGTCATGA
TGCAGTTGATGCGAAGATTACCTTCGGCAGCGGCATGACCGTTGACTTCACCCAGGTTAG
CAACAATGTGGATATTAAGGGCGCGACGGTATCCGCCGAAGATATGAACACTGCGTTAAC
CGGTCAGGCTTATACCGTAGCTAACGGCGCACAGTCTTATGACGTTGCCGCTGATGGTGC
AGTAACTGCTACTACAGGTGGAGCGACCGTAAATATTGGTGCTGAGGGTGAACTGACGAC
TGCGGCCAACAAGACTGTCACAGAAACTTATCACGAATTTGCTAACGGCAATATTCTGGA
TGATGACGGCGCGGCTCTGTATAAAGCGGCTGACGGCTCTCTGACCACTGAAGCTACAGG
TAAATCTGAAGCGACCACGGATCCGCTGAAAGCGCTGGACGATGCTATCGCATCCGTAGA
CAAATTCCGTTCTTCCCTGGGTGCCGTGCAGAACCGTCTGGATTCCGCAGTCACCAACCT
GAACAACACCACTACCAACCTGTCCGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGC
GACCGAAGTGTCCAACATGTCGAAAGCGCAGATTATTCAGCAGGCAGGTAACTCCGTGCT
GGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 36

AACAAAAACCAGTCTGCGCTGTCGACTTCTAT
CGAGCGCCTCTCTTCTGGTCTGCGCATTAACAGCGCTAAAGATGACGCTGCGGGCCAGGC
GATTGCTAACCGCTTCACTTCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAA
CGACGGTATCTCTCTGGCGCAGACCACTGAAGGCGCACTGTCTGAAATCAACAACAACTT
GCAGCGTGTGCGTGAGTTGACTGTTCAGGCGACGACCGGGACTAACTCTGATTCTGACCT
GTCTTCTATTCAGGACGAAATCAAATCCCGTCTGGATGAAATTGACCGTGTTTCCGGTCA
GACCCAGTTCAACGGCGTGAACGTGCTGGCTAAAAACGGTTCTATGGCGATTCAGGTTGG
CGCGAATGATGGGCAGACCATCAACATCGACCTGCAGAAAATCGACTCTTCTACTCTGGG
CCTGGGCGGCTTCTCCGTATCTAACAATGCACTGAAACTGAGCGATTCTATCACTCAGGT
TGGTGCGAGTGGTTCACTGGCAGATGTGAAACTGAGCTCTGTTGCCTCGGCTCTGGGTGT
AGACGCAAGCACTCTGACTCTGCACAACGTACAGACCCCAGCTGGCGCAGCAACAGCTAA
CTATGTTGTCTCTTCTGGTTCTGACAACTACTCAGTATCTGTTGAAGATAGCTCCGGTAC
AGTTACGCTGAACACCACTGATATAGGTTATACCGATACCGCTAATGGCGTTACTACCGG
TTCCATGACTGGTAAGTACGTTAAAGTTGGAGCTGATGCATTGGGTGCTGCTGTAGGTTA
TGTCACCGTACAGGGACAAAACTTCAAAGCTGATGCTGGCGCGCTGGTTAACTCCAAGAA
TGCTGCTGGTAGTCAGAATGTTACTTCTGCAATTGGCGATATTGCTAATAAAGCGAATGC
TAACATTTACACTGGAACCTCTTCTGCAGATCCACTGGCTCTGCTGGACAAAGCTATCGC
ATCTGTTGATAAATTCCGTTCTTCTCTAGGGGCGGTGCAGAACCGTCTGAGCTCTGCTGT
AACCAACCTGAACAACACCACTACCAACCTGTCCGAAGCGCAGTCCCGTATTCAGGACGC
CGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATCATCCAGCAGGCGGGTAA
CTCCGTGCTGTCTAAA

Figure 37

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCA
CTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTT
CTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCCGGTCAGGCGATTGCTAACCGTT
TTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAATGACGGTATTTCTG
TTGCACAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATTCGTG
AACTGACGGTTCAGGCTTCTACCGGGACTAACTCTGATTCGGATCTGGACTCCATTCAGG
ACGAAATCAAATCCCGTCTCGACGAAATTGACCGCGTATCCGGTCAGACCCAGTTCAACG
GCGTGAACGTACTGGCAAAAGACGGTTCGATGAAAATTCAGGTTGGTGCGAACGACGGCC
AGACTATCACTATTGATCTGAAGAAAATTGACTCTGATACGCTGGGGCTGAGTGGGTTTA
ACGTAAATGGTAGCGCAGATAAGGCAAGTGTCGCGGCGACAGCTGACGGAATGGTTAAAG
ACGGATATATCAAAGGGTTAACTTCATCTGACGGCAGCACTGCATATACTAAAACTACAG
CAAATACTGCAGCAAAAGGATCTGATATTCTTGCGGCGCTTAAGACTGGCGATAAAATTA
CCGCAACAGGTGCAAATAGCCTTGCTGATAATGCGACATCGACAACTTATACTTATAATG
CAACCAGCAATACCTTCTCCTATACGGCTGACGGTGTAAACCAAACGAATGCTGCAGCAA
ATCTCATACCTGCAGCAGGGAAAACGACAGCTGCATCAGTTACTATTGGTGGGACAGCAC
AGAATGTAAATATTGATGATTCGGGCAATATTACTTCAAGTGATGGCGATCAACTTTATC
TGGATTCAACAGGTAACCTGACTAAAAACCAGGCCGGCAACCCGAAAAAAGCAACCGTTT
CTGGGCTTCTCGGAAATACGGATGCGAAAGGTACTGCTGTTAAAACAACCATCAAGACAG
AGGCTGGTGTAACAGTTACAGCTGAAGGTAATACAGGTACTGTAAAAATTGAAGGTGCTA
CTGTTTCAGCATCTGCATTTACGGGCATTGCATATTCCGCCAACACCGGTGGGAATACTT
ATGCTGTTGCCGCAAATAATACTACAAATGGTTTCCTGGCGGGGGATGACTTAACCCAGG
ATGCTCAAACTGTTTCAACCTACTACTCGCAAGCCGATGGCACGGTCACGAATAGCGCAG
GCAAAGAAATCTATAAAGACGCTGATGGTGTCTACAGCACAGAGAATAAAACATCGAAGA
CGTCCGATCCATTGGCTGCGCTTGACGACGCAATCAGCTCCATCGACAAATTCCGTTCAT
CCTTGGGTGCTATCCAGAACCGTCTGGATTCCGCGGTCACCAACCTGAACAACACCACTA
CCAACCTGTCCGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCA
ACATGTCGAAAGCGCAGATCATCCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCTAACC
AGGTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGCTAA

Figure 38

AACAAATCTCAGTCTTCTCTGAGCTCCGCCATTGAACGTCTCTCTTCTGGCCTGCGTA
TTAACAGTGCTAAAGATGACGCAGCAGGTCAGGCGATTGCTAACCGTTTTACAGCAAATA
TTAAAGGTCTGACTCAGGCTTCCCGTAACGCGAATGATGGTATTTCTGTTGCGCAGACCA
CTGAAGGTGCGCTGAATGAAATTAACAACAACCTGCAGCGTGTACGTGAACTGACTGTTC
AGGCAACTAACGGTACTAACTCTGACAGCGATCTTTCTTCTATCCAGGCTGAAATTACTC
AACGTCTGGAAGAAATTGACCGTGTATCTGAGCAAACTCAGTTTAACGGCGTGAAAGTCC
TTGCTGAAAATAATGAAATGAAAATTCAGGTTGGTGCTAATGATGGTGAAACCATCACTA
TCAATCTGGCAAAAATTGATGCGAAAACTCTCGGCCTGGACGGTTTTAATATCGATGGCG
CGCAGAAAGCAACTGGCAGTGACCTGATTTCTAAATTTAAAGCGACAGGTACTGATAACT
ATGATGTTGGCGGTGATGCTTATACTGTTAACGTAGATAGCGGAGCTGGGTAATGACTCC
AACTTATTGATAGTGTTTTATGTTCAGATAATGCCCGATGACTTTGTCATGCAGCTCCAC
CGATTTTGAGAACGACAGCGACTTCCGTCCCAGCCGTGCCAGGTGCTGCCTCAGATTCAG
GTTATGCCGCTCAATTCGCTGCGTATATCGCTTGCTGATTACGTGCAGCTTTCCCTTCAG
GCGGGATTCATACAGCGGCCAGCCATCCGTCATCCATATCACCACGTCAAAGGGTGACAG
CAGGCTCATAAGACGCCCCAGCGTCGCCATAGTGCGTTCACCGAATACGTGCGCAACAAC
CGTCTTCCGGAGCCTGTCATACGCGTAAAACAGCCAGCGCTGGCGCGATTTAGCCCCGAC
ATAGTCCCACTGTTCGTCCATTTCCGCGCAGACGATGACGTCACTGCCCGGCTGTATGCG
CGAGGTTACCGACTGCGGCCTGAGTTTTTTAAGTGACGTAAAATCGTGTTGAGGCCAACG
CCCATAATGCGGGCAGTTGCCCGGCATCCAACGCCATTCATGGCCATATCAATGATTTTC
TGGTGCGTACCGGGTTGAGAAGCGGTGTAAGTGAACTGCAGTTGCCATGTTTTACGGCAG
TGAGAGCAGAGATAGCGCTGATGTCCGGCGGTGCTTTTGCCGTTACGCACCACCCCGTCA
GTAGCTGAACAGGAGGGACAGCTGATAGAAACAGAAGCCACTGGAGCACCTCAAAAACAC
CATCATACACTAAATCAGTAAGTTGGCAGCATTACCGCGGAGCTGTTAAAGATACTACAG
GGAATGATATTTTTGTTAGTGCAGCAGATGGTTCACTGACAACTAAATCTGACACAAACA
TAGCTGGTACAGGGATTGATGCTACAGCACTCGCAGCAGCGGCTAAGAATAAAGCACAGA
ATGATAAATTCACGTTTAATGGAGTTGAATTCACAACAACAACTGCAGCGGATGGCAATG
GGAATGGTGTATATTCTGCAGAAATTGATGGTAAGTCAGTGACATTTACTGTGACAGATG
CTGACAAAAAAGCTTCTTTGATTACGAGTGAGACAGTTTACAAAAATAGCGCTGGCCTTT
ATACGACAACCAAAGTTGATAACAAGGCTGCCACACTTTCCGATCTTGATCTCAATGCAG
CTAAGAAAACAGGAAGCACGTTAGTTGTTAACGGTGCAACTTACGATGTTAGTGCAGATG
GTAAAACGATAACGGAGACTGCTTCTGGTAACAATAAAGTCATGTATCTGAGCAAATCAG
AAGGTGGTAGCCCGATTCTGGTAAACGAAGATGCAGCAAAATCGTTGCAATCTACCACCA
ACCCGCTCGAAACTATCGACAAAGCATTGGCTAAAGTTGACAATCTGCGTTCTGACCTCG
GTGCAGTACAAAACCGTTTCGACTCTGCTATCACCAACCTTGGCAACACCGTAAACAACC
TGTCTTCTGCCCGTAGCCGTATCGAAGATGCTGACTACGCGACCGAAGTGTCTAACATGT
CTCGTGCGCAGATCCTGCAACAAGCGGGTACCTCTGTTCTGGCGCAG

Figure 39

AACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGT
CTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACC
GTTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTT
CTGTTGCGCAGACCACCGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTGTGC
GTGAACTGACCGTTCAGGCAACCACCGGTACCAACTCCCAGTCTGACCTGGACTCTATCC
AGGACGAAATTAAATCCCGTCTGGACGAAATTGACCGCGTATCCGGTCAGACCCAGTTCA
ACGGCGTGAACGTACTGGCAAAAGACGGTTCCATGAAAATTCAGGTTGGCGCGAACGATG
GCCAGACCATCACTATCGACCTGAAGAAGATTGACTCTTCTACGCTGAAACTGACTGGTT
TTAACGTGAATGGCAAAGCAGCGGTTGATAATGCTAAAGCGACGGATGCAAATCTGACTA
CCGCCGGTTTTACACAAGGCGTTGTGGATTCAAATGGTAATAGTACTTGGACTAAATCAA
CTACGACTAATTTCGATGCGGCAACTGCAGTAAACGTACTAGCAGCAGTTAAAGATGGCA
GCACAATCAATTACACCGGTACTGGTAATGGTTTAGGGATTGCTGCAACAAGTGCTTATA
CATATCACGATAGCACTAAATCCTATACCTTTGATTCTACGGGGGCTGCAGTAGCTGGTG
CCGCGTCCAGCCTGCAAGGTACTTTTGGTACAGATACGAATACTGCAAAAATCACCATCG
ATGGTTCTGCTCAAGAAGTAAACATCGCTAAAGATGGGAAAATTACTGATACTGATGGTA
AAGCTTTATATATCGATTCCACTGGTAATTTGACTAAGAACGGCTCTGATACTTTAACTC
AGGCAACATTGAATGATGTCCTTACTGGTGCTAATTCAGTTGATGATACAAGGATTGACT
TCGATAGCGGCATGTCTGTCACCCTTGATAAAGTGAACAGCACTGTAGATATCACTGGCG
CATCTATTTCAGCCGCTGCAATGACTAATGAGTTGACAGGTAAGGCCTATACCGTAGTAA
ATGGTGCAGAATCTTACGCTGTAGCTACTAATAACACAGTAAAAAACGACTGCTGATGCTA
AAAATGTTTATGTTGATGCTAGTGGTAAATTAACTACTGATGACAAAGCCACTGTTACAG
AAACTTATCATGAATTTGCGAATGGCAATATCTATGATGATAAAGGCGCTGCTGTTTATG
CGGCGGCGGATGGTTCTCTGACTACAGAAACTACAAGTAAATCAGAAGCTACAGCTAACC
CGCTGGCCGCTCTGGACGACGCAATCAGCCAGATCGACAAATTCCGTTCATCCCTGGGTG
CTATCCAGAACCGTCTGGATTCCGCAGTCACCAACCTGAACAACACCACTACCAATCTGT
CTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAATATGTCGA
AAGCGCAGATCATCCAGCAGGCAGGCAACTCCGTGCTGGCAAAA

Figure 40

AACAAAAACCAGTCTGCGCTGTCGACTTCTATCGAGCGCCTCTC
TTCTGGTCTGCGCATTAACAGCGCTAAAGATGACGCTGCGGGCCAGGCGATTGCTAACCG
CTTCACTTCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAACGACGGTATCTC
TCTGGCGCAGACCACTGAAGGCGCACTGTCTGAAATCAACAACAACTTGCAGCGTGTTCG
TGAACTGACCGTTCAGGCCACTACCGGTACTAACTCTGATTCTGACCTGTCTTCAATCCA
GGACGAAATCAAATCCCGTCTCGATGAAATTGACCGCGTATCCGGTCAGACTCAGTTCAA
CGGCGTGAACGTACTGGCAAAAGATGGCTCGATGAAAATTCAGGTCGGTGCAAATGATGG
TCAGACAATCAGCATTGATTTGCAGAAGATTGATTCTTCTACTTTAGGGTTAAATGGTTT
TTCTGTTTCCAAAAATGCAGTATCTGTTGGTGATGCTATTACTCAATTGCCTGGCGAGAC
GGCAGCCGATGCACCAGTAACCATCAAGTTTGATGATTCAGTAAAAACTGATTTAAAACT
GACCGATGCTTCAGGGTTAAGTCTGCATAACCTCAAAGATGAAAATGGTAATTTAACTAA
CCAGTATGTTGTACAGAATGGCGGAAAATCTTACGCTGCTACAGTCGCTGCCAATGGTAA
TGTTACGCTGAACAAAGCAAATGTAACCTACAGCGATGTCGCAAACGGTATTGATACCGC
AACGCAGTCAGGCCAGTTAGTTCAGGTTGGTGCAGATTCTACCGGTACGCCAAAAGCATT
CGTGTCTGTCCAAGGTAAAAGCTTTGGCATTGATGACGCCGCCTTGAAGAATAACACTGG
TGATGCTACCGCTACTCAACCGGGAACATCTGGGACAACAGTTGTCGCAGCGTCAATTCA
TCTGAGTACGGGCAAAAACTCTGTAGACGCTGATGTAACGGCTTCCACTGAATTCACAGG
TGCTTCAACCAACGATCCACTGACTCTGCTGGACAAAGCTATCGCATCTGTTGATAAATT
CCGTTCTTCTTTGGGGGCGGTACAGAACCGTCTGAGCTCCGCTGTAACCAACCTGAACAA
CACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGA
AGTGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCAGGTAACTCCGTGCTGTCCAA A

Figure 41

AACAAAAACCAGTCTGCGCTGTCGACTTCTATCGAGCGCCTCTCTTCTGGTC
TGCGCATTAACAGCGCTAAAGATGACGCTGCGGGCCAGGCGATTGCTAACCGCTTCACTT
CTAACATCAAAGGTCTGACTCAGGCTGCACGTAACGCCAATGACGGTATTTCTCTAGCAC
AGACAGCGGAAGGCGCGCTGTCAGAGATTAACAACAACTTGCAGCGTGTGCGTGAGTTGA
CCGTGCAGGCAACCACTGGTACCAACTCTGATTCCGATCTCTCTTCTATTCAGGATGAAA
TTAAATCTCGTCTGGATGAAATTGACCGCGTCTCTGGTCAGACCCAGTTTAACGGCGTGA
ACGTACTGGCTAAAAACGGTTCTATGGCAATTCAGGTTGGCGCGAACGATGGCCAGACTA
TCTCTATCGACCTGCAGAAAATAGACTCTTCTACTCTGGGTCTGAGCGGCTTCTCTGTTT
CTCAGAACTCCCTGAAACTGAGCGATTCTATCACTACGATCGGCAATACTACTGCTGCAT
CGAAGAACGTGGACCTGAGCGCAGTAGCAACTAAACTGGGCGTGAATGCAAGCACCCTGA
GCCTGCACGAAGTTCAGGACTCTGCTGGTGACGGTACTGGTACCTTCGTTGTTTCTTCTG
GCAGCGACAACTATGCTGTGTCTGTAGACGCGGCCTCTGGTGCAGTTAACCTGAACACCA
CTGACGTCACCTATGATGACGCTACTAATGGTGTTACTGGCGCGACTCAGAACGGTCAGC
TGATCAAAGTAACTTCTGACGCCAACGGTGCAGCTGTTGGTTACGTAACCATTCAGGGTA
AAAACTATCAGGCTGGTGCGACCGGTGTTGACGTTCTGGCGAACAGCGGTGTTGCAGCTC
CAACTACAGCTGTTGATACCGGTACTCTGCAACTGAGCGGTACTGGTGCAACTACTGAGC
TGAAAGGTACTGCAACTCAGAACCCACTGGCACTATTGGACAAAGCTATCGCTTCTGTTG
ATAAATTCCGTTCTTCTCTGGGTGCGGTACAGAATCGTCTGAGCTCTGCTGTAACCAACC
TGAATAACACCACCACTAACCTGTCTGAAGCGCAGTCCCGTATTCAGGATGCCGACTATG
CGACCGAAGTGTCAAATATGTCTAAAGCGCAGATCGTTCAGCAGGCCGGTAAC

Figure 42

AACAAATCTCAGTCTTCTCTTAGCTCTGCTATTGAGCGTCTGTCTTCT
GGTCTGCGTATTAACAGCGCAAAAGACGATGCAGCAGGTCAGGCGATTGCTAACCGTTTT
ACGGCAAATATTAAAGGTCTGACCCAGGCTTCCCGTAACGCAAATGATGGTATTTCTGTT
GCGCAGACCACTGAAGGTGCGCTGAATGAAATTAACAACAACCTGCAGCGTATTCGTGAA
CTTTCTGTTCAGGCAACTAACGGTACTAACTCTGACAGCGATCTTTCTTCTATCCAGGCT
GAAATTACTCAACGTCTGGAAGAAATTGACCGTGTATCTGAGCAAACTCAGTTTAACGGC
GTGAAAGTCCTTGCTGAAAATAATGAAATGAAAATTCAGGTTGGTGCTAATGATGGTGAA
ACCATCACTATCAATCTGGCAAAAATTGATGCGAAAACTCTCGGCCTGGACGGTTTTAAT
ATCGATGGCGCGCAGAAAGCAACAGGCAGTGACCTGATTTCTAAATTTAAAGCGACAGGT
ACTGATAATTATGATGTTGGCGGTAAAACTTATACCGTGAATGTGGAGAGCGGCGCGGTT
AAGAATGATGCTAATAAAGATGTTTTTGTAAGCGCAGCTGATGGATCGCTGACGACCAGT
AGTGATACTAAAGTATCCGGTGAAAGTATTGATGCAACAGAACTAGCGAAACTTGCAATA
AAATTAGCTGACAAAGGCTCCATTGAATACAAGGGCATTACATTTACTAACAACACTGGC
GCAGAGCTTGATGCTAATGGTAAAGGTGTTTTGACCGCAAATATTGATGGTCAAGATGTT
CAATTTACTATTGACAGTAATGCACCCACGGGTGCCGGCGCAACAATAACTACAGACACA
GCTGTTTACAAAAACAGTGCGGGCCAGTTCACCACTACAAAAGTGGAAAATAAAGCCGCA
ACACTCTCTGATCTGGATCTTAATGCAGCCAAGAAAACAGGTAGCACTTTAGTTGTAAAT
GGCGCCACCTACAATGTCAGCGCAGATGGTAAAACGGTAACTGATACTACTCCTGGTGCC
CCTAAAGTGATGTATCTGAGCAAATCAGAAGGTGGTAGCCCGATTCTGGTAAACGAAGAT
GCAGCAAAATCGTTGCAATCTACCACCAACCCGCTCGAAACTATCGACAAGGCATTGGCT
AAAGTTGACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACCGTTTCGACTCTGCCATC
ACCAACCTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTAGCCGTATCGAAGATGCT
GACTACGCGACCGAAGTGTCTAACATGTCTCGTGCGCAGATCCTGCAACAAGCGGGTACC
TCTGTTCTGGCGCAG

Figure 43

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACT
CAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCT
GGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTC
ACCTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGTT
GCACAGACCACCGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATCCGTGAA
CTGACGGTTCAGGCTTCTACCGGGACTAACTCTGATTCGGATCTGGACTCCATTCAGGAC
GAAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCCGGCCAGACCCAGTTCAACGGC
GTGAACGTGCTGGCGAAAGACGGTTCAATGAAAATTCAGGTTGGTGCGAATGACGGCCAG
ACTATCACTATTGATCTGAAGAAAATTGACTCTGATACTCTGGGTTTGAGTGGATTTAAT
GTGAATGGCAAAGGGGCTGTGGCTAACGCAAAAGCGACCGAAGCAGATTTAACGGGGGCT
GGTTTCTCTCAAGGAGCGGTGGATACAAACGGAAATAGTACTTGGACAAAATCAACCACC
ACCAATTACTCAGCTGCAACAACTGCTGACTTGTTATCGACCATTAAGGATGGCTCTACT
GTTACATATGCAGGGACAGACACCGGATTAGGGGTCGCAGCAGCAGGAAATTATACTTAT
GATGCGAACAGTAAATCTTATTCCTTCAATGCCAATGGTCTGACGGGCGCAAATACCGCA
ACTGCACTCAAAGGTTACTTGGGGACAGGTGCTAACACCGCTAAAATTTCTATCGGTGGT
ACAGAGCAGGAAGTGAATATTGCCAAAGATGGCACTATTACAGATACGAATGGTGATGCG
CTCTATCTGGATATTACCGGCAACCTGACTAAGAACTATGCGGGTTCACCACCTGCAGCA
ACGCTGGATAACGTATTAGCTTCCGCAACTGTAAATGCCACTATCAAGTTTGATAGCGGT
ATGACGGTTGATTACACTGCAGGTACTGGCGCGAATATTACAGGTGCATCCATTTCTGCA
GATGACATGGCCGCAAAACTGAGCGGAAAGGCGTACACTGTTGCCAATGGTGCTGAGTCT
TATGACGTTGCTGCAGTTACGGGGGCTGTAACAACTACAGCAGGTAATTCACCTGTGTAT
GCCGATGCAGACGGTAAATTAACGACGAGTGCCAGTAATACGGTTACTCAGACTTATCAC
GAGTTTGCTAATGGTAACATTTATGATGACAAAGGCTCGTCACTGTATAAAGCTGCAGAT
GGCTCTCTGACTTCTGAAGCTAAAGGGAAATCTGAAGCAACCGCCGATCCCCTGAAAGCT
CTGGACGAAGCCATCAGCTCCATCGACAAATTCCGCTCCTCCCTCGGTGCCGTTCAAAAC
CGTCTGGATTCTGCGGTGACCAACCTGAACAACACCACTACCAACCTGTCTGAAGCGCAG
TCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAATATGTCGAAAGCGCAGATC
ATCCAGCAGGCCGGTAACTCCGTGTTGGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTG
TCTCTGCTGCAGGGTTAA

Figure 44

GCGCTGTCGACTTCTATCGAGCGCCTCTCTTCTGGTTTGCGCATTAACAGCGCTA
AAGATGACGCTGCGGGCCAGGCGATTGCTAACCGCTTCACTTCTAACATCAAAGGTCTGA
CTCAGGCCGCACGTAACGCCAACGACGGTATCTCTCTGGCGCAGACCACTGAAGGCGCAC
TGTCTGAAATCAACAACAACTTGCAGCGTGTTCGTGAACTGACCGTTCAGGCCACTACCG
GTACTAACTCTGATTCTGACCTGTCTTCAATCCAGGACGAAATCAAATCCCGCTTGGCTG
AAATCGATCGTGTCTCTGGTCAGACCCAGTTCAACGGCGTGAACGTGCTGGCTAAAAACG
GTTCTCTGAATATTCAGGTTGGCGCGAATGATGGGCAGACCATCTCTATCGATTTGCAGA
AAATAGACTCTTCTGCCCTTGGTTTAAGTGGTTTTAGTGTTGCCGGTGGGGCGCTAAAAT
TAAGCGATACAGTGACGCAGGTCGGCGATGGTTCAGCCGCGCCAGTTAAAGTGGATCTGG
ATGCAGCAGCAACAGATATTGGTACTGCTTTGGGGCAAAAGGTTAATGCAAGTTCTTTAA
CGTTGCACAATATCTTAGACAAAGATGGTGCGGCAACTGAGAACTATGTTGTTAGCTATG
GTAGTGATAATTACGCTGCATCTGTTGCAGATGACGGGACTGTAACTCTTAATAAAACGG
ATATTACTTATTCAGGCGGTGATATTACCGGCGCTACCAAAGATGATACGTTGATTAAAG
TTGCTGCTAATTCTGACGGAGAGGCCGTTGGTTTCGCTACCGTTCAGGGTAAGAATTATG
AAATTACAGATGGTGTAAAAAACCAGTCCACTGCTGCACCAACCGATATTGCTCAGACCA
TTGATCTGGATACGGCTGATGAATTTACTGGGGCTTCCACTGCTGATCCACTGGCACTTT
TAGACAAAGCTATTGCACAGGTTGATACTTTCCGCTCCTCCCTCGGTGCCGTTCAAAACC
GTCTGGATTCCGCAGTCACCAACCTGAACAACACTACTACCAACCTGTCTGAAGCGCAGT
CCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAATATGTCGAAAGCGCAGATCA TCCAGCAGGCC

Figure 45

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACT
CAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCT
GGCTTGCGTATTAACAGCGCGAAGGATGACGCAGCGGGTCAGGCGATTGCTAACCGTTTT
ACTTCTAATATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAATGACGGTATTTCTCTG
GCGCAGACCACTGAAGGCGCACTGTCTGAAATCAACAACAACTTGCAGCGTGTGCGTGAA
CTGACCGTACAGGCGACAACCGGAACGAACTCCGAATCTGACCTGTCCTCTATCCAGGAC
GAAATCAAATCCCGTCTGGAAGAGATTGACCGCGTATCCGGCCAGACTCAGTTCAACGGC
GTGAATGTGCTGGCAAAAGACGGCACCATGAAAATTCAGGTAGGCGCGAACGATGGTCAG
ACTATCTCTATCGATCTGAAAAAAATCGACTCTTCAACCCTGGGCCTGACCGGTTTTGAT
GTTTCGACGAAAGCGAATATTTCTACGACAGCAGTAACGGGGGCGGCAACGACCACTTAT
GCTGATAGCGCCGTTGCAATTGATATCGGAACGGATATTAGCGGTATTGCTGCTGATGCT
GCGTTAGGAACGATCAATTTCGATAATACAACAGGCAAGTACTACGCACAGATTACCAGT
GCGGCCAATCCGGGCCTTGATGGTGCTTATGAAATCCATGTTAATGACGCGGATGGTTCC
TTCACTGTAGCAGCGAGTGATAAACAAGCGGGTGCTGCTCCGGGTACTGCTCTGACAAGC
GGTAAAGTTCAGACTGCAACCACCACGCCAGGTACGGCTGTTGATGTCACTGCGGCTAAA
ACTGCTCTGGCTGCAGCAGGTGCTGACACGAGTGGCCTGAAACTGGTTCAACTGTCCAAC
ACGGATTCCGCAGGTAAAGTGACCAACGTGGGTTACGGCCTGCAGAATGACAGCGGCACT
ATCTTTGCAACCGACTACGATGGCACCACTGTGACCACGCCGGGCGCAGAGACTGTGACT
TACAAAGATGCTTCCGGTAACAGCACCACTGCGGCTGTCACACTGGGTGGCTCTGATGGC
AAAACCAATCTGGTTACCGCCGCTGACGGCAAAACGTACGGTGCGACTGCACTGAATGGT
GCTGATCTGTCCGATCCTAATAACACCGTTAAATCTGTTGCAGACAACGCTAAACCGTTG
GCTGCCCTGGATGATGCAATTGCGATGGTCGACAAATTCCGCTCCTCCCTCGGTGCGGTG
CAAAACCGTCTGGATTCCGCAGTCACCAACCTGAACAACACCACTACCAACCTGTCTGAA
GCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCG
CAGATTATCCAGCAGGCAGGTAACTCCGTGCTGTCCAAAGCTAACCAGGTTCCGCAGCAG
GTTCTGTCTCTGCTGCAGGGTTAA

Figure 46

AACAAAAACCAGTCTGCGCTGTCGACTTCTATCGAGCGCCTCTCTTCTGGT
CTGCGTATTAACAGCGCTAAAGATGACGCCGCGGGCCAGGCGATTGCTAACCGCTTTACT
TCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAACGACGGTATTTCTCTGGCG
CAGACGGCTGAAGGCGCGCTGTCAGAGATTAACAACAACTTGCAGCGTATTCGTGAACTG
ACCGTTCAGGCCTCTACCGGCACGAACTCTGATTCCGACCTGTCTTCTATTCAGGACGAA
ATCAAATCCCGTCTTGATGAAATTGACCGTGTATCTGGTCAGACCCAGTTCAACGGTGTG
AACGTGCTGTCGAAAAACGATTCGATGAAGATTCAGATTGGTGCCAATGATAACCAGACG
ATCAGCATTGGCTTGCAACAAATCGACAGTACCACTTTGAATCTGAAAGGATTTACCGTG
TCCGGCATGGCGGATTTCAGCGCGGCGAAACTGACGGCTGCTGATGGTACAGCAATTGCT
GCTGCGGATGTCAAGGATGCTGGGGGTAAACAAGTCAATTTACTGTCTTACACTGACACC
GCGTCTAACAGTACTAAATATGCGGTCGTTGATTCTGCAACCGGTAAATACATGGAAGCC
ACTGTAGCCATTACCGGTACGGCGGCGGCGGTAACTGTTGGTGCAGCGGAAGTGGCGGGA
GCCGCTACAGCCGATCCGTTAAAAGCACTGGATGCCGCAATCGCTAAAGTCGACAAATTC
CGCTCCTCCCTCGGTGCCGTTCAAAACCGTCTGGATTCTGCGGTCACCAACCTGAACAAC
ACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAA
GTGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCCGGTAACTCCGTGCTGGCAAA

Figure 47

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTC
AAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTG
GCTTGCGTATTAACAGCGCGAAGGATGACGCAGCGGGTCAGGCGATTGCTAACCGTTTTA
CCTCTAACATTAAAGGTCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGTTG
CACAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTATCCGTGAAC
TGACGGTTCAGGCTTCTACCGGGACTAACTCCGATTCGGATCTGGACTCCATTCAGGACG
AAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCCGGTCAAACCCAGTTCAACGGTG
TGAACGTACTGGCGAAAGACGGTTCGATGAAAATTCAGGTTGGTGCGAATGACGGCCAGA
CTATCACGATTGATCTGAAGAAAATTGACTCAGATACGCTGGGGCTGAATGGTTTCAACG
TTAATGGCAAAGGCACTATTGCGAACAAAGCTGCTACAGTCAGCGATCTGACCGCTGCTG
GTGCAACGGGAACAGGTCCTTATGCTGTGACCACAAACAATACAGCACTCAGCGCTAGCG
ATGCACTGTCTCGCCTGAAAACCGGAGATACAGTTACTACTACTGGCTCGAGTGCTGCGA
TCTATACTTATGATGCGGCTAAAGGGAACTTCACCACTCAAGCAACAGTTGCAGATGGCG
ATGTTGTTAACTTTGCGAATACTCTGAAACCAGCGGCTGGCACTACTGCATCAGGTGTTT
ATACTCGTAGTACTGGTGATGTGAAGTTTGATGTAGATGCTAATGGCGATGTGACCATCG
GTGGTAAAGCCGCGTACCTGGACGCCACTGGTAACCTATCTACAAACAACCCCGGCATTG
CATCTTCAGCGAAATTGTCCGATCTGTTTGCTAGCGGTAGTACCTTAGCGACAACTGGTT
CTATCCAGCTGTCTGGCACAACTTATAACTTTGGTGCAGCGGCAACTTCTGGCGTAACCT
ACACCAAAACTGTAAGCGCTGATACTGTACTGAGCACAGTGCAGAGTGCTGCAACGGCTA
ACACAGCAGTTACTGGTGCGACAATTAAGTATAATACAGGTATTCAGTCTGCAACGGCGT
CCTTCGGTGGTGTGAATACTAATGGTGCTGGTAATTCGAATGACACCTATACTGATGCAG
ACAAAGAGCTCACCACAACCGCATCTTACACTATCAACTACAACGTCGATAAGGATACCG
GTACAGTAACTGTAGCTTCAAATGGCGCAGGTGCAACTGGTAAATTTGCAGCTACTGTTG
GGGCACAGGCTTATGTTAACTCTACAGGCAAACTGACCACTGAAACCACCAGTGCAGGCA
CTGCAACCAAAGATCCTCTGGCTGCCCTGGATGAAGCTATCAGCTCCATCGACAAATTCC
GTTCATCCCTGGGTGCTATCCAGAACCGTCTGGATTCCGCGGTTACCAACCTGAACAACA
CCACTACCAACCTGTCCGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAG
TGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCCGGTAACTCCGTGCTGGCAAAAG
CCAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 48

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCAC
TCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTC
TGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTT
TACTTCTAATATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAATGACGGTATTTCTGT
TGCACAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTGTGCGTGA
ACTGACCGTTCAGGCGACCACCGGTACCAACTCCCAGTCTGATCTGGACTCTATCCAGGA
CGAAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCCGGTCAGACTCAGTTCAACGG
CGTGAACGTACTGGCAAAAGACGGTTCCATGAAAATTCAGGTTGGCGCGAATGATGGCCA
GACCATCACTATCGACCTGAAGAAGATTGACTCTTCTACGTTGAAACTGACTGGTTTTAA
CGTGAATGGTTCTGGTTCTGTGGCGAATACTGCGGCGACTAAAGACGAACTGGCTGCTGC
TGCTGCGGCGGCGGGTACAACTCCTGCTGTCGGTACTGACGGCGTGACCAAATATACCGT
AGACGCAGGGCTTAACAAAGCCACAGCAGCAAACGTGTTTGCAAACCTTGCAGATGGTGC
TGTTGTTGATGCTAGCATTTCCAACGGTTTTGGTGCAGCAGCAGCCACAGACTACACCTA
CAATAAAGCTACAAATGATTTCACTTTCAATGCCAGCATTGCTGCTGGTGCTGCGGCCGG
TGATAGTAACAGCGCAGCTCTGCAATCCTTCCTGACTCCAAAAGCAGGTGATACAGCTAA
CCTGAGCGTCAAAATCGGTACGACATCTGTTAATGTTGTTCTGGCGAGCGATGGCAAAAT
TACAGCGAAAGATGGCTCAGCTCTGTATATCGACTCAACGGGTAACCTGACTCAGAACAG
CGCAGGCACTGTAACAGCAGCAACCCTGGATGGACTGACCAAAAACCATGATGCGACAGG
AGCTGTTGGTGTTGATATCACGACCGCAGATGGCGCAACTATCTCTCTGGCAGGCTCTGC
TAACGCGGCAACAGGTACTCAATCAGGTGCAATTACACTGAAAAATGTTCGTATCAGTGC
TGATGCTCTGCAGTCTGCTGCGAAAGGTACTGTTATCAATGTTGATAATGGTGCTGATGA
TATTTCTGTTAGTAAAACCGGGTGTCGTTACTACCGGAGGTGCGCCTACTTATACTGATG
CTGATGGTAAATTAACGACAACCAACACCGTTGATTATTTCCTGCAAACTGATGGCAGCG
TAACCAATGGTTCTGGTAAAGGGGTTTACACCGATGCAGCTGGTAAATTCACTACCGACG
CTGCAACCAAAGCCGCAACCACCACCGATCCGCTGAAAGCCCTTGATGACGCAATCAGCC
AGATCGATAAGTTCCGTTCATCCCTGGGTGCTATCCAGAACCGTCTGGATTCCGCGGTTA
CCAACCTGAACAACACCACTACCAACCTGTCCGAAGCGCAGTCCCGTATTCAGGACGCCG
ACTATGCGACCGAAGTGTCCAATATGTCGAAAGCGCAGATCATCCAGCAGGCCGGTAACT
CCGTGTTGGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 49

AACAAATCTCAGTCTTCTCTTAGCTCTGCTATTGAGCGTCTGTCTTCTGGT
CTGCGTATTAACAGCGCAAAAGACGATGCAGCAGGTCAGGCGATTGCTAACCGTTTTACG
GCAAATATTAAAGGTCTGACCCAGGCTTCCCGTAACGCGAATGATGGTATTTCTGTTGCG
CAGACCACTGAAGGTGCGCTGAATGAAATTAACAACAACCTGCAGCGTATTCGTGAACTT
TCTGTTCAGGCAACTAACGGTACTAACTCTGACAGCGATCTTTCTTCTATCCAGGCTGAA
ATTACTCAACGTCTGGAAGAAATTGACCGTGTATCTGAGCAAACTCAGTTTAACGGCGTG
AAAGTCCTTGCTGAAAATAATGAAATGAAAATTCAGGTTGGTGCTAATGATGGTGAAACC
ATCACTATCAATCTGGCAAAAATTGATGCGAAAACTCTCGGCCTGGACGGTTTTAATATC
GATGGCGCGCAGAAAGCAACCGGCAGTGACCTGATTTCTAAATTTAAAGCGACAGGTACT
GATAATTATCAAATTAACGGTACTGATAACTATACTGTTAATGTAGATAGTGGAGTAGTA
CAGGATAAAGATGGCAAACAAGTTTATGTGAGTGCTGCGGATGGTTCACTTACGACCAGC
AGTGATACTCAATTCAAGATTGATGCAACTAAGCTTGCAGTGGCTGCTAAAGATTTAGCT
CAAGGTAATAAGATTGTCTACGAAGGTATCGAATTTACAAATACCGGCACTGGCGCTATA
CCTGCCACAGGTAATGGTGAATTAACCGCCAATGTTGATGGTAAGGCTGTTGAATTCACT
ATTTCGGGGAGTGCTGATACATCAGGTACTAGTGCAACCGTTGCCCCTACGACAGCCCTA
TACAAAAATAGTGCAGGGCAATTGACTGCAACAAAAGTTGAAAATAAAGCAGCGACACTA
TCTGATCTTGATCTGAACGCTGCCAAGAAAACAGGAAGCACGTTAGTTGTTAACGGTGCA
ACTTACGATGTTAGTGCAGATGGTAAAACGATAACGGAGACTGCTTCTGGTAACAATAAA
GTCATGTATCTGAGCAAATCAGAAGGTGGTAGCCCGATTCTGGTAAACGAAGATGCAGCA
AAATCGTTGCAATCTACCACCAACCCGCTCGAAACTATCGACAAAGCATTGGCTAAAGTT
GACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACCGTTTCGACTCTGCCATCACCAAC
CTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTAGCCGTATCGAAGATGCTGACTAC
GCGACCGAAGTGTCTAACATGTCTCGTGCGCAGATCCTGCAACAAGCGGGTACCTCTGTT CTGGCACAG

Figure 50

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCAC
TCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCCTCTGTCTTC
TGGCTTGCGTATTAACAGCGCGAAGGATGACGCAGCGGGTCAGGCGATTGCTAACCGTTT
CACCTCTAACATTAAAGGCCTGACTCAGGCGGCCCGTAACGCCAACGACGGTATCTCCGT
TGCGCAGACCACCGAAGGCGCGCTGTCCGAAATCAACAACAACTTACAGCGTGTGCGTGA
ACTGACGGTACAGGCCACTACCGGTACTAACTCTGAGTCTGATCTGTCTTCTATCCAGGA
CGAAATTAAATCCCGTCTGGATGAAATTGACCGCGTATCTGGTCAGACCCAGTTCAACGG
CGTGAACGTGCTGGCAAAAAATGGCTCCATGAAAATCCAGGTTGGCGCAAATGATAACCA
GACTATCACTATCGATCTGAAGCAGATTGATGCTAAAACTCTTGGCCTTGATGGTTTTAG
CGTTAAAAATAACGATACAGTTACCACTAGTGCTCCAGTAACTGCTTTTGGTGCTACCAC
CACAAACAATATTAAACTTACTGGAATTACCCTTTCTACGGAAGCAGCCACTGATACTGG
CGGAACTAACCCAGCTTCAATTGAGGGTGTTTATACTGATAATGGTAATGATTACTATGC
GAAAATCACCGGTGGTGATAACGATGGGAAGTATTACGCAGTAACAGTTGCTAATGATGG
TACAGTGACAATGGCGACTGGAGCAACGGCAAATGCAACTGTAACTGATGCAAATACTAC
TAAAGCTACAACTATCACTTCAGGCGGTACACCTGTTCAGATTGATAATACTGCAGGTTC
CGCAACTGCCAACCTTGGTGCTGTTAGCTTAGTAAAACTGCAGGATTCCAAGGGTAATGA
TACCGATACATATGCGCTTAAAGATACAAATGGCAATCTTTACGCTGCGGATGTGAATGA
AACTACTGGTGCTGTTTCTGTTAAAACTATTACCTATACTGACTCTTCCGGTGCCGCCAG
TTCTCCAACCGCGGTCAAACTGGGCGGAGATGATGGCAAAACAGAAGTGGTCGATATTGA
TGGTAAAACATACGATTCTGCCGATTTAAATGGCGGTAATCTGCAAACAGGTTTGACTGC
TGGTGGTGAGGCTCTGACTGCTGTTGCAAATGGTAAAACCACGGATCCGCTGAAAGCGCT
GGACGATGCTATCGCATCTGTAGACAAATTCCGTTCTTCCCTCGGTGCGGTGCAAAACCG
TCTGGATTCCGCGGTTACCAACCTGAACAACACCACTACCAACCTGTCTGAAGCGCAGTC
CCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAATATGTCGAAAGCGCAGATCAT
CCAGCAGGCCGGTAACTCCGTGTTGGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTGTC
TCTGCTGCAGGGTTAA

Figure 51

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACT
CAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCT
GGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTT
ACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTCTGTT
GCGCAGACCACCGAAGGCGCGCTGTCTGAAATCAACAACAACTTACAGCGTATTCGTGAA
CTGACGGTTCAGGCTTCTACCGGGACTAACTCTGATTCGGATCTGGACTCCATTCAGGAC
GAAATCAAATCCCGTCTGGACGAAATTGACCGCGTATCCGGTCAAACCCAGTTCAACGGT
GTGAACGTACTGGCGAAAGACGGTTCGATGAAAATTCAGGTTGGTGCGAATGACGGCCAG
ACTATCACTATTGATCTGAAGAAAATTGACTCTGATACGCTGGGGCTGAATGGTTTTAAC
GTTAACGGCAAAGGTACTATTGCGAACAAAGCGGCAACCATTAGTGATCTGGCGGCGACG
GGGGCGAATGTTACTAACTCAAGCAATATTGTTGTCACGACAAAGTTCAATGCCTTGGAT
GCAGCGACTGCATTTAGCAAACTCAAAGATGGTGATTCTGTTGCCGTTGCTGCTCAGAAA
TATACTTATAACGCATCGACCAATGATTTTACGACAGAAAATACAGTAGCGACAGGCACT
GCAACGACAGATCTTGGCGCTACTCTGAAGGCTGCTGCTGGGCAGAGTCAATCAGGTACA
TATACCTTTGCAAATGGTAAAGTTAACTTTGATGTTGATGCAAGCGGTAATATCACTATT
GGCGGCGAAAAGGCTTTCTTGGTTGGTGGAGCGCTGACTACTAACGATCCCACCGGCTCC
ACTCCAGCAACGATGTCTTCCCTGTTTAAGGCCGCGGATGACAAAGATGCCGCTCAATCC
TCGATTGATTTTGGCGGGAAAAAATACGAATTTGCTGGTGGCAATTCTACTAATGGTGGC
GGCGTTAAATTCAAAGACACGGTGTCTTCTGACGCGCTTTTGGCTCAGGTTAAAGCGGAT
AGTACTGCTAATAATGTAAAAATCACCTTTAACAATGGTCCTCTGTCATTCACTGCATCG
TTCCAAAATGGTGTATCTGGCTCCGCGGCATCGAATGCAGCCTACATTGATAGCGAAGGC
GAACTGACAACTACTGAATCCTACAACACAAATTATTCCGTAGACAAAGACACGGGGGCT
GTAAGTGTTACAGGGGGGGAGCGGTACGGGTAAATACGCCGCAAACGTGGGTGCTCAGGCT
TATGTAGGTGCAGATGGTAAATTAACCACGAATACTACTAGTACCGGCTCTGCAACCAAA
GATCCACTAAATGCGCTGGATGAGGCAATTGCATCCATCGACAAATTCCGTTCTTCCCTG
GGGGCTATCCAGAACCGTCTGGATTCCGCAGTCACCAACCTGAACAACACCACTACCAAC
CTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAACATG
TCGAAAGCGCAGATCATCCAGCAGGCCGGTAACTCCGTGTTGGCAAAAGCTAACCAGGTA
CCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 52

AACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTC
TTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCGGGTCAGGCGATTGCTAACCG
TTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACGACGGTATTTC
TGTTGCGCAGACCACCGAAGGCGCGCTGTCCGAAATTAACAACAACTTACAGCGTGTGCG
TGAGCTGACTGTTCAGGCGACCACCGGTACTAACTCTGAGTCTGACCTGTCTTCTATCCA
GGACGAAATCAAATCTCGCCTGGAAGAGATTGATCGTGTTTCAAGTCAGACTCAATTTAA
CGGCGTGAATGTTTTGGCTAAAGATGGGAAAATGAACATTCAGGTTGGGGCAAGTGATGG
ACAGACTATCACTATTGATCTGAAAAAGATCGATTCATCTACACTAAACCTCTCCAGTTT
TGATGCTACAAACTTGGGCACCAGTGTTAAAGATGGGGCCACCATCAATAAGCAAGTGGC
AGTAGATGCTGGCGACTTTAAAGATAAAGCTTCAGGATCGTTAGGTACCCTAAAATTAGT
TGAGAAAGACGGTAAGTACTATGTAAATGACACTAAAAGTAGTAAGTACTACGATGCCGA
AGTAGATACTAGTAAGGGTGAAATTAACTTCAACTCTACAAATGAAAGTGGAACTACTCC
TACTGCAGCGACGGAAGTAACTACTGTTGGCCGCGATGTAAAATTGGATGCTTCTGCACT
TAAAGCCAACCAATCGCTTGTCGTGTATAAAGATAAAAGCGGCAATGATGCTTATATCAT
TCAGACCAAAGATGTAACAACTAATCAATCAACTTTCAATGCCGCTAATATCAGTGATGC
TGGTGTTTTATCTATTGGTGCATCTACAACCGCGCCAAGCAATTTAACAGCTGACCCGCT
TAAGGCTCTTGATGATGCAATTGCATCTGTTGATAAATTCCGCTCTTCTCTCGGTGCCGT
TCAGAACCGTCTGGATTCTGCCATTGCCAACCTGAACAACACCACTACCAACCTGTCTGA
AGCGCAGTCCCGTATTCAGGACGCTGACTATGCGACCGAAGTGTCCAACATGTCGAAAGC
GCAGATTATCCAGCAGGCCGGTAACTCCGTGCTGGCAAAA

Figure 53

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAA
TAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTT
GCGTATTAACAGCGCGAAGGATGACGCAGCGGGTCAGGCGATTGCTAACCGTTTCACCTC
TAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCTAACGATGGTATCTCTCTGGCGCA
GACCACTGAAGGCGCACTGTCTGAGATTAACAACAACTTACAACGTGTGCGTGAGTTGAC
TGTACAGGCGACCACCGGTACTAACTCTGATTCTGACCTGGCTTCTATTCAGGACGAAAT
CAAATCCCGTTTGTCTGAAATTGACCGCGTATCCGGGCAGACCCAGTTCAACGGCGTGAA
CGTATTGTCTAAAGATGGCTCCCTGAAAATTCAGGTTGGCGCAAATGATGGTCAGACTAT
CTCTATCGACCTGAAGAAAATTGACTCTGATACTCTGGGTTTGAATGGTTTCAACGTTAA
TGGTTCTGGTACCATTGCAAACAAAGCGGCCACAATCAGTGACTTGACTGCTCAGAAAGC
CGTTGACAACGGTAATGGTACTTATAAAGTTACAACTAGCAACGCTGCACTTACTGCATC
TCAGGCATTAAGTAAGCTGAGTGATGGCGATACTGTAGATATTGCAACCTATGCTGGTGG
TACAAGTTCAACAGTTAGTTATAAATACGACGCAGATGCAGGTAACTTCAGTTATAACAA
TACTGCAAACAAAACAAGTGCTGCGGCTGGAACTCTGGCAGATACTCTTCTCCCGGCAGC
TGGCCAGACTAAAACCGGTACTTACAAGGCTGCTACTGGTGATGTTAACTTTAATGTTGA
CGCAACTGGTAATCTGACAATTGGCGGACAGCAAGCCTACCTGACTACTGATGGTAACCT
TACAACAAACAACTCCGGTGGTGCGGCTACTGCAACTCTTAAAGAGCTGTTTACTCTTGC
TGGCGATGGTAAATCTCTGGGGAACGGCGGTACTGCTACCGTTACTCTGGATAATACTAC
GTATAATTTCAAAGCTGCTGCGAACGTTACTGATGGTGCTGGTGTCATCGCTGCTGCTGG
TGTAACTTATACAGCCACTGTTTCTAAAGATGTCATTCTGGCACAACTGCAATCTGCAAG
TCAGGCAGCAGCAACCGCTACCGACGGTGATACTGTCGCAACGATCAACTATAAATCTGG
TGTCATGATCGGTTCCGCTACCTTTACCAATGGTAAAGGTACTGCCGATGGTATGACTTC
TGGTACAACTCCAGTCGTAGCTACAGGTGCTAAAGCTGTATATGTTGATGGCAACAATGA
ACTGACTTCCACTGCATCTTACGATACGACTTACTCTGTCAACGCAGATACAGGCGCAGT
AAAAGTGGTATCAGGTACTGGTACTGGTAAATTTGAAGCTGTTGCTGGTGCGGATGCTTA
TGTAAGCAAAGATGGCAAATTAACGACAGAAACCACCAGTGCAGGCACTGCAACCAAAGA
TCCTTTGGCTGCCCTGGATGCTGCTATCAGCTCCATCGACAAATTCCGTTCCTCCCTGGG
TGCTATCCAGAACCGTCTGGATTCCGCAGTCACCAACCTGAACAACACCACTACTAACCT
GTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAATATGTC
GAAAGCGCAGATCATCCAGCAGGCCGGTAACTCTGTGTTGGCAAAAGCTAACCAGGTACC
GCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 54

ATGGCACAAGTCATTAATACCAACAGCC
TCTCGCTGATCACTCAAAATAATATCAACAAGAACCAGTCTGCGCTGTCGAGTTCTATCG
AGCGTCTGTCTTCTGGCTTGCGTATTAACAGCGCGAAGGATGACGCCGCAGGTCAGGCGA
TTGCTAACCGTTTTACTTCTAACATTAAAGGCCTGACTCAGGCTGCACGTAACGCCAACG
ACGGTATTTCTGTTGCACAGACCACTGAAGGCGCGCTGTCCGAAATCAACAACAACTTAC
AGCGTATTCGTGAACTGACGGTTCAGGCTTCTACCGGGACTAACTCTGATTCGGATCTGG
ACTCCATTCAGGACGAAATCAAATCCCGTCTCGACGAAATTGACCGCGTTTCCGGTCAGA
CCCAGTTCAACGGCGTGAACGTGCTGGCGAAAGACGGTTCGATGAAGATTCAGGTTGGCG
CGAATGACGGGCAGACCATCTCTATCGATTTGCAGAAAATTGATTCTTCAACGCTGGGAT
TGAAAGGTTTCTCGGTATCAGGGAACGCATTAAAAGTTAGCGATGCGATAACTACAGTTC
CTGGTGCTAATGCTGGCGATGCCCCGGTTACGGTTAAATTTGGTGCGAACGATACCGCTG
CTGCCGCAATGGCTAAAACATTGGGAATAAGTGATACATCAGGCTTGTCCCTACATAACG
TACAAAGCGCGGATGGTAAAGCGACAGGAACCTATGTTGTTCAATCTGGTAATGACTTCT
ATTCGGCTTCCGTTAATGCTGGTGGCGTTGTTACGCTTAATACCACCAATGTTACTTTCA
CTGATCCTGCGAACGGTGTTACCACAGCAACACAGACAGGTCAGCCTATCAAGGTCACGA
CGAATAGTGCTGGCGCGGCTGTTGGCTATGTTACTATTCAAGGCAAAGATTACCTTGCTG
GTGCAGACGGTAAGGATGCAATTGAAAACGGTGGTGACGCTGCAACAAATGAAGACACAA
AAATCCAACTTACCGATGAACTCGATGTTGATGGTTCTGTAAAAACAGCGGCAACAGCAA
CATTTTCTGGTACTGCAACCAACGATCCGCTGGCACTTTTAGACAAAGCTATCTCGCAAG
TTGATACTTTCCGCTCCTCCCTCGGTGCCGTACAAAACCGTCTGGATTCTGCGGTCACCA
ACCTGAATAACACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACT
ATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATCATCCAGCAGGCGGGTAACTCTG
TGCTGTCTAAAGCTAACCAGGTACCGCAGCAGGTTCTGTCTCTGCTGCAGGGTTAA

Figure 55

CTTCTCTTAGCTCTGCTATTGAGCGTCTGTCTTCTGGTCTGCGTATTAACAGCGCAAAAG
ACGATGCAGCAGGTCAGGCGATTGCTAACCGTTTTACGGCAAATATTAAAGGTCTGACCC
AGGCTTCCCGTAACGCGAATGATGGTATTTCTGTTGCGCAGACCACTGAAGGTGCGCTGA
ATGAAATTAACAACAACCTGCAGCGTATTCGTGAACTTTCTGTTCAGGCAACTAACGGTA
CTAACTCTGACAGCGATCTTTCTTCTATCCAGGCTGAAATTACTCAACGTCTGGAAGAAA
TTGACCGTGTATCTGAGCAAACTCAGTTTAACGGCGTGAAAGTCCTTGCTGAAAATAATG
AAATGAAAATTCAGGTTGGTGCTAATGATGGTGAAACCATTGACCTGCCCCCACGATTAG
ATACAACACTCAGTTAGTAACGTCGGAATCTTCATTCTCAGAATGACCCTTTCTCCAGCC
CGCTGCAAATTCAGACGGTGTCTGATAATTCAGCGTGGAGTGCGGGCGGCATTCGTTATA
ATCCTGCCGCCAGTCATTAATAATTTTCCTGGCATGAACGATATCGCTGAACCAGTGCTC
ATTCAAACATTCATCGCGAAATCGTCCGTTAAAGCTCTCAATAAATCCGTTCTGCGTTGG
CTTGCCCGGCTGGATTAAGCGCAACTCAACACCATGCTCAAAGGCCCATTGATCCAGTGC
ACGGCAAGTGAACTCCGGCCCCTGGTCAGTTCTTATCGTCGCCGGATAGCCTCGAAACAG
TGCAATGCTGTCCAGAATACGCGTGACCTGAACGCCTGAAATCCCAAAGGCAACAGTGAC
CGTCAGGCATTCCTTTGTGAAATCATCGACGCAGGTAAGACACTTGATCCTGCGACCGGT
GGAAAGTGCGTCCATGACGAAATCCATCGACCAGGTCAGATTGGGCGCCGCCGGACGGAG
CAGCGGCAGACGTTCTGTTGCCAGCCCTTTACGACGTCTTCTGCGTTTTACGCCCAGGCC
ACTGAGGTGATAAAGCCGGTACACGCGCTTATGATTAACATGAAGCCCTTCACGGCGCAG
CAACTGCCAAATACGACGGTAGCCAAAACGCCTGCGCTCCAGTGCCAGCTCAGTGATGCG
CCCTGATAAATGCGCATCAGCAGCCGGACGGTGAGCCTCATAGCGGCAGGTCGACAGGGA
TAAACCTGTAAGCCTGCAGGCACGACGTTGCGACAGACCGGTCGCATCACACATCAACAT
CACGGCTTCCCGCTTCTGGTCTGTCGTCAGTACTTTCGCCCAAGAGCCACCTGAAGCGCC
TCTTTATCCAGCATGGCTTCGGCAAGCAGCTTCTTGAGTCTGGTGTTCTCTTCCTCAAGC
GACTTCAGGCGCTTAACTTCAGGCACCTCCATACCGCCATACTTCTTACGCCAGGTGTAA
AACGTGGCATCGGAAATGGCATGCTTGCGGCAGAGTTCACGGGCGGGTACCCCAGCTTCG
GCTTCGCGGAGAATACTGATGATCTGTTCGTCGGAAAAACGCTTCTTCATGGGGATGTCC
TCATGTGGCTTATGAAGACATTACTAACATCGGGGTGTACTAATCAACGGGGAGCAGGTC
ACCATCACTATCAATCTGGCAAAAATTGATGCGAAAACTCTCGGCCTGGACGGTTTTAAT
ATCGATGGCGCGCAGAAAGCAACCGGCAGTGACCTGATTTCTAAATTTAAAGCGACAGGT
ACTGATAATTATCAAATTAACGGTACTGATAACTATACTGTTAATGTAGATAGTGGAGTA
GTACAGGATAAAGATGGCAAACAAGTTTATGTGAGTGCTGCGGATGGTTCACTTACGACC
AGCAGTGATACTCAATTCAAGATTGATGCAACTAAGCTTGCAGTGGCTGCTAAAGATTTA
GCTCAAGGTAATAAGATTGTCTACGAAGGTATCGAATTTACAAATACCGGCACTGGCGCT
ATACCTGCCACAGGTAATGGTAAATTAACCGCCAATGTTGATGGTAAGGCTGTTGAATTC
ACTATTTCGGGGAGTGCTGATACATCAGGTACTAGTGCAACCGTTGCCCCTACGACAGCC
CTATACAAAAATAGTGCAGGGCAATTGACTGCAACAAAAGTTGAAAATAAAGCAGCGACA
CTATCTGATCTTGATCTGAACGCTGCCAAGAAAACAGGAAGCACGTTAGTTGTTAACGGT
GCAACTTACGATGTTAGTGCAGATGGTAAAACGATAACGGAGACTGCTTCTGGTAACAAT
AAAGTCATGTATCTGAGCAAATCAGAAGGTGGTAGCCCGATTCTGGTAAACGAAGATGCA
GCAAAATCGTTGCAATCTACCACCAACCCGCTCGAAACTATCGACAAAGCATTGGCTAAA
GTTGACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACCGTTTCGACTCTGCCATCACC
AACCTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTAGCCGTATCGAAGATGCTGAC
TACGCGACCGAAGTGTCTAACATGTCTCGTGCGCAGATCCTGCAACAAGCGGGTACCTCT
GTTCTGGCACAGGCTAACC

Figure 56

AACAAAAACCAGTCTGCGCTGTCGACTTCTATCGAGCGCCTCTCT
TCTGGTCTGCGCATTAACAGCGCTAAAGATGACGCTGCGGGCCAGGCGATTGCTAACCGC
TTCACTTCTAACATCAAAGGTCTGACTCAGGCCGCACGTAACGCCAACGACGGTATCTCT
CTGGCGCAGACCACTGAAGGCGCACTGTCTGAAATCAACAACAACTTGCAGCGTGTTCGT
GAACTGACCGTTCAGGCCACTACCGGTACTAACTCTGATTCTGACCTGTCTTCAATCCAG
GACGAAATCAAATCCCGTCTCGATGAAATTGACCGCGTATCCGGTCAGACTCAGTTCAAC
GGCGTGAACGTACTGGCAAAAGATGGCTCGATGAAAATTCAGGTCGGTGCAAATGATGGT
CAGACAATCAGCATTGATTTGCAGAAGATTGATTCTTCTACTTTAGGGTTAAATGGTTTT
TCTGTTTCCAAAAATGCAGTATCTGTTGGTGATGCTATTACTCAATTGCCTGGCGAGACG
GCAGCCGATGCACCAGTAACCATCAAGTTTGATGATTCAGTAAAAACTGATTTAAAACTG
ACCGATGCTTCAGGGTTAAGTCTGCATAACCTCAAAGATGAAAATGGTAATTTAACTAAC
CAGTATGTTGTACAGAATGGCGGAAAATCTTACGCTGCTACAGTCGCTGCCAATGGTAAT
GTTACGCTGAACAAAGCAAATGTAACCTACAGCGATGTCGCAAACGGTATTGATACCGCA
ACGCAGTCAGGCCAGTTAGTTCAGGTTGGTGCAGATTCTACCGGTACGCCAAAAGCATTC
GTGTCTGTCCAAGGTAAAAGCTTTGGCATTGATGACGCCGCCTTGAAGAATAACACTGGT
GATGCTACCGCTACTCCACCGGGAACATCTGGACAACAGTTGTCGCAGCGTCAATTCAT
CTGAGTACGGGCAAAAACTCTGTAGACGCTGATGTAACGGCTTCCACTGAATTCACAGGT
GCTTCAACCAACGATCCACTGACTCTGCTGGACAAAGCTATCGCATCTGTTGATAAATTC
CGTTCTTCTTTGGGGGCGGTACAGAACCGTCTGAGCTCCGCTGTAACCAACCTGAACAAC
ACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCAGGACGCCGACTATGCGACCGAA
GTGTCCAACATGTCGAAAGCGCAGATTATCCAGCAGGCAGGTAACTCCGTGCTGTCCAAA

Figure 57

AACAAAAACCAGTCTGCGCTGTCGACTTCTATCGAACGCCTCTCTTCTGG
CCTGCGTATTAACAGTGCGAAAGATGACGCTGCCGGTCAGGCGATAGCTAACCGTTTCAC
CTCTAACATTAAAGGCCTGACTCAGGCTGCGCGTAACGCCAACGACGGTATTTCTCTGGC
GCAGACCACAGAAGGTGCGTTGTCTGAAATCAACAACAACTTGCAACGTGTGCGTGAGTT
GACCGTTCAGGCGACGACCGGTACTAACTCTGATTCTGACCTGTCATCTATTCAGGACGA
AATCAAATCCCGTCTGGATGAGATTGACCGTGTTTCCGGTCAGACCCAGTTCAACGGCGT
GAATGTACTGGCAAAAGACGGTTCGATGAAGATTCAGGTTGGCGCGAATGATGGCCAGAC
TATTAGCATTGATTTACAGAAAATTGACTCTTCTACATTAGGGTTGAATGGTTTCTCCGT
TTCTGCTCAATCACTTAACGTTGGTGATTCAATTACTCAAATTACAGGAGCCGCTGGGAC
AAAACCTGTTGGTGTTGATTTCACTGCTGTTGCGAAAGATCTGACTACTGCGACAGGTAA
AACTGTCGATGTTTCCAGCCTGACGTTACACAACACCCTGGATGCGAAAGGGGCTGCCAC
CGCACAGTTCGTCGTTCAATCCGGTAGTGATTTCTACTCCGCGTCCATTGACCATGCAAG
TGGTGAAGTGACGTTGAATAAAGCCGATGTCGAATACAAAGACACCGATAATGGACTAAC
GACTGCAGCTACTCAGAAAGATCAGCTGATTAAAGTTGCCGCTGACTCTGACGGCGCGGC
TGCGGGATATGTAACATTCCAGGGTAAAAACTACGCTACAACGGCTCCAGCGGCGCTTAA
TGATGACACTACGGCAACAGCCACAGCGAACAAAGTTGTTGTTGAATTATCTACAGCAAC
TCCGACTGCGCAGTTCTCAGGGGCTTCTTCTGCTGATCCACTGGCACTTTTAGACAAAGC
CATTGCACAGGTTGATACTTTCCGCTCCTCCCTCGGTGCCGTTCAAAACCGTCTGGACTC
TGCGGTAACCAACCTGAACAACACCACCACCAACCTGTCTGAAGCGCAGTCCCGTATTCA
GGACGCCGACTATGCGACCGAAGTGTCTAACATGTCGAAAGCGCAGATCATCCAGCAGGC
GGGTAACTCTGTGCTGTCTAAA

Figure 58

ATGCCACAAG TCATTAATAC CAACAGCCTC TCGCTGATCA CTCAAAATAA TATCAACAAG
AACCAGTCTG CGCTGTCGAG TTCTATCGAG CGTCTGTCTT CTGGCTTGCG TATTAACAGC
GCGAAGGATG ACGCCGCGGG TCAGGCGATT GCTAACCGTT TTACTTCTAA CATTAAAGGC
CTGACTCAGG CTGCACGTAA CGCCAACGAC GGTATTTCTG TTGCACAGAC CACTGAAGGC
GCGCTGTCCG AAATCAACAA CAACTTACAG CGTATCCGTG AGCTGACGGT TCAGGCTTCT
ACCGGGACTA ACTCTGATTC GGATCTGGAC TCCATTCAGG ACGAAATCAA ATCCCGTCTC
GACGAAATTG ACCGCGTATC CGGTCAGACC CAGTTCAACG GCGTGAACGT ACTGGCAAAA
GACGGTTCGA TGAAAATTCA GGTTGGTGCG AATGACGGTG AAACTATCAC TATCGACCTG
AAGAAAATCG ATTCTGATAC TCTGGGTCTG AATGGTTTTA ACGTAAATGG TAAAGGTACT
ATTACCAACA AAGCTGCAAC GGTAAGTGAT TTAACTTCTG CTGGCGCGAA GTTAAACAC
CACGACAGGT CTTTATGATC TGAAAACCGA AAATACCTTG TTAACTACCG ATGCTGCATT
CGATAAATTA GGGAATGGCG ATAAAGTCAC CGTTGGCGGC GTAGATTATA CTTACAACGC
TAAATCTGGT GATTTTACTA CCACCAAATC TACTGCTGGT ACGGGTGTAG ACGCCGCGGC
GCAGGCTACT GATTCAGCTA AAAAACGTGA TGCGTTAGCT GCCACCCTTC ATGCTGATGT
GGGTAAATCT GTTAATGGTT CTTACACCAC AAAAGATGGT ACTGTTTCTT TCGAAACGGA
TTCAGCAGGT AATATCACCA TCGGTGGAAG CCAGGCATAC GTAGACGATG CAGGCAACTT
GACGACTAAC AACGCTGGTA GCGCAGCTAA AGCTGATATG AAAGCGCTGC TTAAAGCCGC
GAGCGAAGGT AGTGACGGTG CCTCTCTGAC ATTCAATGGC ACTGAATATA CTATCGCAAA
AGCAACTCCT GCGACAACCT CTCCAGTAGC TCCGTTAATC CCTGGTGGGA TTACTTATCA
GGCTACAGTG AGTAAAGATG TAGTATTGAG CGAAACCAAA GCGGCTGCCG CGACATCTTC
AATTACCTTT AATTCCGGTG TACTGAGCAA AACTATTGGG TTTACCGCGG GTGAATCCAG
TGATGCTGCG AAGTCTTATG TGGATGATAA AGGTGGTATT ACTAACGTTG CCGACTATAC
AGTCTCTTAC AGCGTTAACA AGGATAACGG CTCTGTGACT GTTGCCGGGT ATGCTTCAGC
GACTGATACC AATAAAGATT ATGCTCCAGC AATTGGTACT GCTGTAAATG TGAACTCCGC
GGGTAAAATC ACTACTGAGA CTACCAGTGC TGGTTCTGCA ACGACCAACC CGCTTGCTGC
CCTGGACGAC GCTATCAGCT CCATCGACAA ATTCCGTTCT TCCCTGGGTG CTATCCAGAA
CCGTCTGGAT TCCGCAGTCA CCAACCTGAA CAACACCACT ACCAACCTGT CTGAAGCGCA
GTCCCGTATT CAGGACGCCG ACTATGCGAC CGAAGTGTCC AACATGTCGA AAGCGCAGAT
TATCCAGCAG GCCGGTAACT CCGTGCTGGC AAAAGCCAAC CAGGTACCGC AGCAGGTTCT
GTCTCTGCTG CAGGGTTAA

Figure 59

ATGGCACAAG TCATTAATAC CAACAGCCTC TCGCTGATCA CTCAAAATAA TATCAACAAG
AACCAGTCTG CGCTGTCGAG TTCTATCGAG CGTCTGTCTT CTGGCTTGCG TATTAACAGC
GCGAAGGATG ACGCCGCAGG TCAGGCGATT GCTAACCGTT TTACTTCTAA CATTAAAGGC
CTGACTCAGG CGGCCCGTAA CGCCAACGAC GGTATTTCTG TTGCGCAGAC CACCGAAGGC
GCGCTGTCCG AAATCAACAA CAACTTACAG CGTATTCGTG AACTGACGGT TCAGGCCACT
ACAGGGACTA ACTCCGATTC TGACCTGGAC TCCATCCAGG ACGAAATCAA ATCTCGTCTT
GATGAAATTG ACCGCGTATC CGGCCAGACC CAGTTCAACG GCGTGAACGT GCTGGCGAAA
GACGGTTCAA TGAAAATTCA GGTTGGTGCG AATGACGGCG AAACCATCAC GATCGACCTG
AAAAAAATCG ATTCTGATAC TCTGGGTCTG AATGGCTTTA ACGTAAATGG TAAAGGTACT
ATTACCAACA AAGCTGCAAC GGTAAGTGAT TTAACTTCTG CTGGCGCGAA GTTAAACAC
CACGACAGGT CTTTATGATC TGAAAACCGA AAATACCTTG TTAACTACCG ATGCTGCATT
CGATAAATTA GGGAATGGCG ATAAAGTCAC AGTTGGCGGC GTAGATTATA CTTACAACGC
TAAATCTGGT GATTTTACTA CCACTAAATC TACTGCTGGT ACGGGTGTAG ACGCCGCGGC
GCAGGCTGCT GATTCAGCTT CAAAACGTGA TGCGTTAGCT GCCACCCTTC ATGCTGATGT
GGGTAAATCT GTTAATGGTT CTTACACCAC AAAAGATGGT ACTGTTTCTT TCGAAACGGA
TTCAGCAGGT AATATCACCA TCGGTGGAAG CCAGGCATAC GTAGACGATG CAGGCAACTT
GACGACTAAC AACGCTGGTA GCGCAGCTAA AGCTGATATG AAAGCGCTGC TCAAAGCAGC
GAGCGAAGGT AGTGACGGTG CCTCTCTGAC ATTCAATGGC ACAGAATATA CCATCGCAAA
AGCAACTCCT GCGACAACCA CTCCAGTAGC TCCGTTAATC CCTGGTGGGA TTACTTATCA
GGCTACAGTG AGTAAAGATG TAGTATTGAG CGAAACCAAA GCGGCTGCCG CGACATCTTC
AATTACCTTT AATTCCGGTG TACTGAGCAA AACTATTGGG TTTACCGCGG GTGAATCCAG
TGATGCTGCG AAGTCTTATG TGGATGATAA AGGTGGTATC ACTAACGTTG CCGACTATAC
AGTCTCTTAC AGCGTTAACA AGGATAACGG CTCTGTGACT GTTGCCGGGT ATGCTTCAGC
GACTGATACC AATAAAGATT ATGCTCCAGC AATTGGTACT GCTGTAAATG TGAACTCCGC
GGGTAAAATC ACTACTGAGA CTACCAGTGC TGGTTCTGCA ACGACCAACC CGCTTGCTGC
CCTGGACGAC GCAATCAGCT CCATCGACAA ATTCCGTTCT TCCCTGGGTG CTATCCAGAA
CCGTCTGGAT TCCGCAGTCA CCAACCTGAA CAACACCACT ACCAACCTGT CCGAAGCGCA
GTCCCGTATT CAGGACGCCG ACTATGCGAC CGAAGTGTCC AACATGTCGA AAGCGCAGAT
CATTCAGCAG GCCGGTAACT CCGTGCTGGC AAAAGCTAAC CAGGTACCGC AGCAGGTTCT
GTCTCTGCTG CAGGGTTAA

Figure 60

ATGGCACAAG TCATTAATAC CAACAGCCTC TCGCTGATCA CTCAAAATAA TATCAACAAG
AACCAGTCTG CGCTGTCGAG TTCTATCGAG CGTCTGTCTT CTGGCTTGCG TATTAACAGC
GCGAAGGATG ACGCAGCGGG TCAGGCGATT GCTAACCGTT TTACTTCTAA CATTAAAGGC
CTGACTCAGG CTGCACGTAA CGCCAACGAC GGTATTTCTG TTGCGCAGAC CACCGAAGGC
GCGCTGTCCG AAATCAACAA CAACTTACAG CGTATTCGTG AACTGACGGT TCAGGCCACT
ACAGGGACTA ACTCCGATTC TGACCTGGAC TCCATCCAGG ACGAAATCAA ATCTCGTCTT
GATGAAATTG ACCGCGTATC CGGCCAGACC CAGTTCAACG GCGTGAACGT GCTGGCGAAA
GACGGTTCAA TGAAAATTCA GGTTGGTGCG AATGACGGCG AAACCATCAC GATCGACCTG
AAAAAAATCG ATTCTGATAC TCTGGGTCTG AATGGCTTTA ACGTAAATGG TAAAGGTACT
ATTACCAACA AAGCTGCAAC GGTAAGTGAT TTAACTTCTG CTGGCGCGAA GTTAAACAC
CACGACAGGT CTTTATGATC TGAAAACCGA AAATACCTTG TTAACTACCG ATGCTGCATT
CGATAAATTA GGGAATGGCG ATAAAGTCAC AGTTGGCGGC GTAGATTATA CTTACAACGC
TAAATCTGGT GATTTTACTA CCACTAAATC TACTGCTGGT ACGGGTGTAA ACGCCGCGGC
GCAGGCTGCT GATTCAGCTT CAAAACGTGA TGCGTTAGCT GCCACCCTTC ATGCTGATGT
GGGTAAATCT GTTAATGGTT CTTACACCAC AAAAGATGGT ACTGTTTCTT TCGAAACGGA
TTCAGCAGGT AATATCACCA TCGGTGGAAG CCAGGCATAC GTAGACGATG CAGGCAACTT
GACGACTAAC AACGCTGGTA GCGCAGCTAA AGCTGATATG AAAGCGCTGC TCAAAGCAGC
GAGCGAAGGT AGTGACGGTG CCTCTCTGAC ATTCAATGGC ACAGAATATA CCATCGCAAA
AGCAACTCCT GCGACAACCA CTCCAGTAGC TCCGTTAATC CCTGGTGGGA TTACTTATCA
GGCTACAGTG AGTAAAGATG TAGTATTGAG CGAAACCAAA GCGGCTGCCG CGACATCTTC
AATTACCTTT AATTCCGGTG TACTGAGCAA AACTATTGGG TTTACCGCGG GTGAATCCAG
TGATGCTGCG AAGTCTTATG TGGATGATAA AGGTGGTATC ACTAACGTTG CCGACTATAC
AGTCTCTTAC AGCGTTAACA AGGATAACGG CTCTGTGACT GTTGCCGGGT ATGCTTCAGC
GACTGATACC AATAAAGATT ATGCTCCAGC AATTGGCACT GCTGTAAATG TGAACTCCGC
GGGTAAAATC ACTACTGAGA CTACCAGTGC TGGTTCTGCA ACGACCAACC CGCTTGCTGC
CCTGGACGAC GCAATCAGCT CCATCGACAA ATTCCGTTCT TCCCTGGGTG CTATCCAGAA
CCGTCTGGAT TCCGCGGTCA CCAACCTGAA CAACACCACT ACCAACCTGT CCGAAGCGCA
GTCCCGTATT CAGGACGCCG ACTATGCGAC CGAAGTGTCC AACATGTCGA AAGCGCAGAT
CATCCAGCAG GCCGGTAACT CCGTGCTGGC AAAAGCTAAC CAGGTACCGC AGCAGGTTCT
GTCTCTGCTG CAGGGTTAA

Figure 61

ATGGCACAAG TCATTAATAC CAACAGCCTC TCGCTGATCA GTCAAAATAA TATCAACAAG
AACCAGTCTG CGCTGTCGAG TTCTATCGAG CGTCTGTCTT CTGGCTTGCG TATTAACAGC
GCGAAGGATG ACGCCGCGGG TCAGGCGATT GCTAACCGTT TTACTTCTAA CATTAAAGGC
CTGACTCAGG CTGCACGTAA CGCCAACGAC GGTATTTCTG TTGCACAGAC CACTGAAGGC
GCGCTGTCCG AAATCAACAA CAACTTACAG CGTATCCGTG AGCTGACGGT TCAGGCTTCT
ACCGGGACTA ACTCTGATTC GGATCTGGAC TCCATTCAGG ACGAAATCAA ATCCCGTCTC
GACGAAATTG ACCGCGTATC CGGTCAGACC CAGTTCAACG GCGTGAACGT ACTGGCAAAA
GACGGTTCGA TGAAAATTCA GGTTGGTGCG AATGACGGTG AAACTATCAC TATCGACCTG
AAGAAAATCG ATTCTGATAC TCTGGGTCTG AATGGTTTTA ACGTAAATGG TAAAGGTACT
ATTACCAACA AAGCTGCAAC GGTAAGTGAT TTAACTTCTG CTGGCGCGAA GTTAAACAC
CACGACAGGT CTTTATGATC TGAAAACCGA AAATACCTTG TTAACTACCG ATGCTGCATT
CGATAAATTA GGGAATGGCG ATAAAGTCAC CGTTGGCGGC GTAGATTATA CTTACAACGC
TAAATCTGGT GATTTTACTA CCACCAAATC TACTGCTGGT ACGGGTGTAG ACGCCGCGGC
GCAGGCTACT GATTCAGCTA AAAAACGTGA TGCGTTAGCT GCCACCCTTC ATGCTGATGT
GGGTAAATCT GTTAATGGTT CTTACACCAC AAAAGATGGT ACTGTTTCTT TCGAAACGGA
TTCAGCAGGT AATATCACCA TCGGTGGAAG CCAGGCATAC GTAGACGATG CAGGCAACTT
GACGACTAAC AACGCTGGTA GCGCAGCTAA AGCTGATATG AAAGCGCTGC TTAAAGCCGC
GAGCGAAGGT AGTGACGGTG CCTCTCTGAC ATTCAATGGC ACTGAATATA CTATCGCAAA
AGCAACTCCT GCGACAACCT CTCCAGTAGC TCCGTTAATC CCTGGTGGGA TTACTTATCA
GGCTACAGTG AGTAAAGATG TAGTATTGAG CGAAACCAAA GCGGCTGCCG CGACATCTTC
AATTACCTTT AATTCCGGTG TACTGAGCAA AACTATTGGG TTTACCGCGG GTGAATCCAG
TGATGCTGCG AAGTCTTATG TGGATGATAA AGGTGGTATT ACTAACGTTG CCGACTATAC
AGTCTCTTAC AGCGTTAACA AGGATAACGG CTCTGTGACT GTTGCCGGGT ATGCTTCAGC
GACTGATACC AATAAAGATT ATGCTCCAGC AATTGGTACT GCTGTAAATG TGAACTCCGC
GGGTAAAATC ACTACTGAGA CTACCAGTGC TGGTTCTGCA ACGACCAACC CGCTTGCTGC
CCTGGACGAC GCTATCAGCT CCATCGACAA ATTCCGTTCT TCCCTGGGTG CTATCCAGAA
CCGTCTGGAT TCCGCAGTCA CCAACCTGAA CAACACCACT ACCAACCTGT CTGAAGCGCA
GTCCCGTATT CAGGACGCCG ACTATGCGAC CGAAGTGTCC AACATGTCGA AAGCGCAGAT
TATCCAGCAG GCCGGTAACT CCGTGCTGGC AAAAGCCAAC CAGGTACCGC AGCAGGTTCT
GTCTCTGCTG CAGGGTTAA

Figure 62

ATGGCACAAGTCATTAATACCAACAGCCTCTCGCTGATCACTCAAAATAATATCAACAAG
AACCAGTCTGCGCTGTCGAGTTCTATCGAGCGTCTGTCTTCTGGCTTGCGTATTAACAGC
GCGAAGGATGACGCCGCAGGTCAGGCGATTGCTAACCGTTTTACTTCTAACATTAAAGGC
CTGACTCAGGCGGCCCGTAACGCCAACGACGGTATTTCTGTTGCGCAGACCACCGAAGGC
GCGCTGTCCGAAATCAACAACAACTTACAGCGTATTCGTGAACTGACGGTTCAGGCCACT
ACAGGGACTAACTCCGATTCTGACCTGGACTCCATCCAGGACGAAATCAAATCTCGTCTT
GATGAAATTGACCGCGTATCCGGCCAGACCCAGTTCAACGGCGTGAACGTGCTGGCGAAA
GACGGTTCAATGAAAATTCAGGTTGGTGCGAATGACGGCGAAACCATCACGATCGACCTG
AAAAAAATCGATTCTGATACTCTGGGTCTGAATGGCTTTAACGTAAATGGTAAAGGTACT
ATTACCAACAAAGCTGCAACGGTAAGTGATTTAACTTCTGCTGGCGCGAAGTTAAACACC
ACGACAGGTCTTTATGATCTGAAAACCGAAAATACCTTGTTAACTACCGATGCTGCATTC
GATAAATTAGGGAATGGCGATAAAGTCACAGTTGGCGGCGTAGATTATACTTACAACGCT
AAATCTGGTGATTTTACTACCACTAAATCTACTGCTGGTACGGGTGTAGACGCCGCGGCG
CAGGCTGCTGATTCAGCTTCAAAACGTGATGCGTTAGCTGCCACCCTTCATGCTGATGTG
GGTAAATCTGTTAATGGTTCTTACACCACAAAAGATGGTACTGTTTCTTTCGAAACGGAT
TCAGCAGGTAATATCACCATCGGTGGAAGCCAGGCATACGTAGACGATGCAGGCAACTTG
ACGACTAACAACGCTGGTAGCGCAGCTAAAGCTGATATGAAAGCGCTGCTCAAAGCAGCG
AGCGAAGGTAGTGACGGTGCCTCTCTGACATTCAATGGCACAGAATATACCATCGCAAAA
GCAACTCCTGCGACAACCACTCCAGTAGCTCCGTTAATCCCTGGTGGGATTACTTATCAG
GCTACAGTGAGTAAAGATGTAGTATTGAGCGAAACCAAAGCGGCTGCCGCGACATCTTCA
ATTACCTTTAATTCCGGTGTACTGAGCAAAACTATTGGGTTTACCGCGGGTGAATCCAGT
GATGCTGCGAAGTCTTATGTGGATGATAAAGGTGGTATCACTAACGTTGCCGACTATACA
GTCTCTTACAGCGTTAACAAGGATAACGGCTCTGTGACTGTTGCCGGGTATGCTTCAGCG
ACTGATACCAATAAAGATTATGCTCCAGCAATTGGTACTGCTGTAAATGTGAACTCCGCG
GGTAAAATCACTACTGAGACTACCAGTGCTGGTTCTGCAACGACCAACCCGCTTGCTGCC
CTGGACGACGCAATCAGCTCCATCGACAAATTCCGTTCTTCCCTGGGTGCTATCCAGAAC
CGTCTGGATTCCGCAGTCACCAACCTGAACAACACCACTACCAACCTGTCCGAAGCGCAG
TCCCGTATTCAGGACGCCGACTATGCGACCGAAGTGTCCAACATGTCGAAAGCGCAGATC
ATTCAGCAGGCCGGTAACTCCGTGCTGGCAAAAGCTAACCAGGTACCGCAGCAGGTTCTG
TCTCTGCTGCAGGGTTAA

Figure 63

ATGGCACAAG TCATTAATAC CAACAGCCTC TCGCTGATCA CTCAAAATAA TATCAACAAG
AACCAGTCTG CGCTGTCGAG TTCTATCGAG CGTCTGTCTT CTGGCTTGCG TATTAACAGC
GCGAAGGATG ACGCCGCAGG TCAGGCGATT GCTAACCGTT TTACTTCTAA CATTAAAGGC
CTGACTCAGG CTGCACGTAA CGCCAACGAC GGTATTTCTG TTGCGCAGAC CACCGAAGGC
GCGCTGTCCG AAATCAACAA CAACTTACAG CGTATTCGTG AACTGACGGT TCAGGCCACT
ACAGGGACTA ACTCCGATTC TGACCTGGAC TCCATCCAGG ACGAAATCAA ATCTCGTCTT
GATGAAATTG ACCGCGTATC CGGCCAGACC CAGTTCAACG GCGTGAACGT GCTGGCGAAA
GACGGTTCAA TGAAAATTCA GGTTGGTGCG AATGACGGCG AAACCATCAC GATCGACCTG
AAAAAAATCG ATTCTGATAC TCTGGGTCTG AATGGCTTTA ACGTAAATGG TAAAGGTACT
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TAAATCTGGT GATTTTACTA CCACTAAATC TACTGCTGGT ACGGGTGTAG ACGCCGCGGC
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AGCAACTCCT GCGACAACCA CTCCAGTAGC TCCGTTAATC CCTGGTGGGA TTACTTATCA
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Figure 64

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GCGCTGTCCG AAATCAACAA CAACTTACAG CGTATCCGTG AGCTGACGGT TCAGGCTTCT
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ATTACCAACA AAGCTGCAAC GGTAAGTGAT TTAACTTCTG CTGGCGCGAA GTTAAACACC
ACGACAGGT CTTTATGATC TGAAAACCGA AAATACCTTG TTAACTACCG ATGCTGCATT
CGATAAATTA GGGAATGGCG ATAAAGTCAC CGTTGGCGGC GTAGATTATA CTTACAACGC
TAAATCTGGT GATTTTACTA CCACCAAATC TACTGCTGGT ACGGGTGTAG ACGCCGCGGC
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Figure 65

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Figure 66

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GAGCGAAGGT AGTGACGGTG CTTCTCTGAC ATTCAATGGC ACTGAATATA CTATCGCAAA
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GGCTACAGTG AGTAAAGATG TAGTATTGAG CGAAACCAAA GCGGCTGCCG CGACATCTTC
AATTACCTTT AATTCCGGTG TACTGAGCAA AACTATTGGG TTTACCGCGG GTGAATCCAG
TGATGCTGCG AAGTCTTATG TGGATGATAA AGGTGGTATT ACTAACGTTG CCGACTATAC
AGTCTCTTAC AGCGTTAACA AGGATAACGG CTCTGTGACT GTTGCCGGGT ATGCTTCAGC
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CCGTCTGGAT TCCGCAGTCA CCAACCTGAA CAACACCACT ACCAACCTGT CTGAAGCGCA
GTCCCGTATT CAGGACGCCG ACTATGCGAC CGAAGTGTCC AACATGTCGA AAGCGCAGAT
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GTCTCTGCTG CAGGGTTAA

Figure 67

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GTCTCTGCTG CAGGGTTAA

Figure 68

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Figure 69

AACAGCCTCTCGCTGATCACTCAGAACAACATCAACAAAAACCAGTCTTC
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Figure 70A

CTCAGTATGCTGTCACCGGCAGTACAGGTGCCGTAACTTACGATCCAGAT
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Figure 70B

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Figure 71

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GTTGACAATCTGCGTTCTGACCTCGGTGCAGTACAAAACCGTTTCGACTCT
GCTATCACCAACCTTGGCAACACCGTAAACAACCTGTCTTCTGCCCGTAGC
CGTATCGAAGATGCTGACTACGCGACCGAAGTGTCTAACATGTCTCGTGC
GCAGATCCTGCAACAAGCGGGTACCTCTGTTCTGGCGCAGGCTAACCAGA
CCACGCAGAACGTAC

Figure 72

FIGURE 73A

Sequence of the polylinker region of plasmid pTrc99A:

$\boxed{\text{AGGA}}$AACAGACC ATG GAA TTC GAG CTC GGT ACC CGG GGA TCC TCT AGA GTC GAC CTG CAG GCA TGC AAG CTT

SD *Nco*I *Eco*RI *Sac*I *Kpn*I *Sma*I *Bam*HI *Xba*I *Sal*I *Pst*I *Sph*I *Hid*III

FIGURE 73B

Sequence in the junction region between vector and the 5' end of the H antigen gene:

*Nco*I

$\boxed{\text{AGGA}}$AACAGACC ATG GCA CAA GTC ATT AAT ACC

SD H antigen gene

SEQUENCE LISTING PART

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<120> ANTIGENS AND THEIR DETECTION

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<140>
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ttaaacctga ctgggtttaa 500

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<213> Escherichia coli

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caaacaaaac tgtaaaatat tatgcccaca ctaatggtag cgtcacgaac gacagtggtt 180
cagctattta cgcaactgaa gcgggcaaat tgactactga agcgtctaca gctgctgaaa 240
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<211> 1689
<212> DNA
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<212> DNA
<213> Escherichia coli

<400> 17

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<213> Escherichia coli

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<211> 1731
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<213> Escherichia coli

<400> 20

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<211> 1380
<212> DNA
<213> Escherichia coli

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<212> DNA
<213> Escherichia coli

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<211> 1197
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<213> Escherichia coli

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<212> DNA
<213> Escherichia coli

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<210> 26
<211> 1365

<212> DNA
<213> Escherichia coli

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<210> 27
<211> 1740
<212> DNA
<213> Escherichia coli

<400> 27
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<210> 28
<211> 1233
<212> DNA
<213> Escherichia coli

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<211> 1713
<212> DNA
<213> Escherichia coli

<400> 29

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<211> 1668
<212> DNA
<213> Escherichia coli

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<210> 31
<211> 1713
<212> DNA
<213> Escherichia coli

<400> 31
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<211> 1188
<212> DNA
<213> Escherichia coli

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<213> Escherichia coli

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<211> 2145
<212> DNA
<213> Escherichia coli

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<211> 1587
<212> DNA
<213> Escherichia coli

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<211> 1245
<212> DNA
<213> Escherichia coli

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<211> 1185
<212> DNA
<213> Escherichia coli

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<212> DNA
<213> Escherichia coli

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<212> DNA
<213> Escherichia coli

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<211> 950
<212> DNA
<213> Escherichia coli

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<213> Escherichia coli

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<213> Escherichia coli

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<211> 14516
<212> DNA
<213> Escherichia coli

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU 99/00385

A. CLASSIFICATION OF SUBJECT MATTER

Int Cl[6]: C07H 21/04, (C12Q 1/10, 1/68, C12R 1:19), G01N 37/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
STN: Chemical Abstracts, Medline and Derwent World Patents Index using keywords e. coli and flagellin
ANGIS: Sequences corresponding to Fig 25, Fig 10 and Fig 34 (random sample)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	JOURNAL OF BACTERIOLOGY, (1999 Jan) 181 (1), Reid S D; Selander R K; Whittam T S, "Sequence diversity of flagellin (fliC) alleles in pathogenic Escherichia coli", 153-160	1-33
X	MOLECULAR MICROBIOLOGY (1994) 12(2), Tominaga A; Mahmoud T; Enomoto M, "Molecular characterization of intact, but cryptic, flagellin genes in the genus Shigella", 277-285	1-33
X	JOURNAL OF MOLECULAR BIOLOGY (1994) 238, Fahrner K A; Block S M; Krishnaswamy S; Parkinson J S; Berg H C, "A mutant hook-associated protein (HAP3) facilitates torsionally induced transformations of the flagellar filament", 173-186	1-33

[X] Further documents are listed in the continuation of Box C

[ ] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
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"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
27 July 1999	-3 AUG 1999

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SCIENCE (Washington DC) (1997) 277(5331), Blattner F R et al, "The complete genome sequence of Escherichia coli K-12", 1453-1462	1-33
X	JOURNAL OF BACTERIOLOGY (Sept. 1993) 175(17), Schoenhals G; Whitfield C, "Comparative analysis of flagellin sequences from Escherichia coli strains possessing serologically distinct flagellar filaments with a shared complex surface pattern", 5395-5402	1-33
X	JOURNAL OF BACTERIOLOGY (Feb. 1998) 180(4), Ratiner Y A, "New flagellin-specifying genes in some Escherichia coli strains", 979-984	1-33
X	FEMS MICROBIOLOGY LETTERS (1987) 48, Ratiner Y A, "Different alleles of the flagellin gene hagB in Escherichia coli standard H test strains", 97-104	1-33
X	FEMS MICROBIOLOGY LETTERS (1985) 29, Ratiner Y A, "Two genetic arrangements determining flagellar antigen specificities in two diphasic Escherichia coli strains", 317-323	1-33